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nr.2040/2
Zea mays histone deacetylase 2 isoform b mRNA, complete cds.
AP254072
                                                                                                                                                                                                          Dangl, M., Brosch, G., Haas, H., Loidl, P. and Lusser, A.
Molecular characterization of type-2 histone deacetylases in higher
                                                                                                                                                                                                                                                                            2 (bases 1 to 912)
Lusser,A. and Loidl,P.
Direct Submission
Submitted (07-APR-2000) Microbiology, Medical School, University of Innsbruck, Fritz-Pregl Str. 3/II, Innsbruck 6020, Austria
Location/Qualifiers
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                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Pred. No. 9.2e-13;
0; Mismatches 217; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="histone deacetylase 2 isoform b"
/protein_id="AAF68624.1"
/db_xref="G1:7716948"
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1. .912
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/organism="Zea mays"
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11.1%;
Best Local Similarity 53.7%;
Matches 266; Conservative
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Search completed: May 2, 2002, 20:13:40 Job time: 15434 sec

355 GAAAATGGCAAAGCTGATGGGAAGGAGGAGCAGAAAAATCAAGAGAAGGCAGTAGCTGCT 414

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Location/Qualifiers
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Best Local Similarity 53.7%;
Matches 267; Conservative
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VNIDDKKLVLGTLSVEKHPQISCDLVFDKDFELPHNSKTRSVFFRGYKSPVPLFESNS
GEDSSDEELKTDQIPLQNNEIKISAKVPAKUDDDDVFIILAMMMITSSDDDDDDFT
TSDSDNEMSEEDDSSDEDENSEEDDSSDEDENSGGADFSDDSSDESGSEHTSAPKKTD
VVOKKRKAIKAARAARARSEOSSGKTGBKASTSHPAKQSIKTPADKSSRKTPTADKS
SPRSGSHGCK"
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                              AF384033 1124 bp mRNA linear PLN 26-JUN-2001
Zea mays HD2 type histone deacetylase HDA106 (hda106) mRNA,
                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 1124)
1 (bases 1 to 1124)
2 handler, V. L., Kaeppler, S. M., Kaeppler, H.F. and Cone, K.C. Sequences from the Plant Chromatin Consortium (NSF Plant Genome project 9975930)
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/protein_id-"AAK67143.1"
/db_xref-"G1:14550106"
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55.2%; Pred. No. 5.8e-14;
tive 0; Mismatches 188;

    1124
    /organism="Zea mays"
    /cultivar="B73"
    /db_xref="taxon:4577"

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Matches 235; Conservative
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PAT 17-DEC-2001
409 TGTTTGAGTCTAATTCTGGTGAAGATAGTTCCGATGAAGAGCTAAAAACCGATCAAATTC 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 ccatggagttctggggaattgaagttaaatcaggaaagccagttacagtgactcctgaag 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 acacttggggaaaaggaagtgtttactttgttggtacaaaact-----ccaacattg
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                                                                              401 ctgccaaggctgtagctaaaccaaaggctaagcctgcagaagtgaagccagctgttgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 aaggcattottatccacgtttctcaggcatcgcttggagaatgtaaaaacaaggagag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 ACACATCGAAAACTACCAGTGTATTTTTCTCTGGTTACAAGGTTGAGCAGCCAATTGAGG
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Baldwin, D.Adelphi., Briggs, S.P. and Crane, V.C.
Maize histone deacetylases and their use
Patent: US 6287843-A 15 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104.2; DB 6;
Pred. No. 7.2e-13;
0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 from patent US 6287843. ARI68370
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SDKKAATAPPSGOKTGDKKGVHVATPHPAKQASKTPVNDKSKEKSPKSGGGSISCKSG
SKTFNSEMALQSHSKAKHPAK"
                                                                                   Dangl,M., Brosch,G., Haas,H., Loidl,P., Graessle,S. and Lusser,A. Molecular characterization of type-2 histone deacetylases in higher
  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 894)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggcattettatecaegttteteaggcategettggagaatgtaaaaaeaagaagggagag 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 atggagttctggggaattgaagttaaatcaggaaagccagttacagtgactcctgaagaa 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GAACGCTTTTTGCACCTTTCTCAGGCTGCTCTTGGGGAAT---CAAAGAAAGGATCTGAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gatgagtetgattetgaeggaatggatgaagatgattetgatggtgaggattetgaggaa 528
                                                                                                                                                                    To (bases 1 to 894)
Dangl.M., Haas,H., Loidl.P. and Lusser,A.
Direct Submission
Submitted (13-APR-2000) Microbiology, University of Innsbruck, Fritz-Pregl-Str. 3, Innsbruck 6020, Austria
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGACTTCTGGGGTCTTGAAGTCAAGCCTGGACCTGTCAAATGTGAGCCTGAAGT
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0; Mismatches 214;
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                                                                                                                                                                                                                                                                                                                      /organism-"oryza sativa'
/db_xref-"dbEST:D15380"
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                                                                                                                                                  Unpublished
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Oryza saliva putative histone deacetylase HD2 mRNA, complete cds.
AF255711
                                                                                                                                                                                   /traislation-*MEWGVEVKNGKPLHLDPGLDRLVHISOVALGESKNNVYPEPIQL
YTVGSDKLLIGTLSHEKFPOLSTEIVLERNKFALSHTWKNGSVFFSGYKUDASDPEPE
DLIDDQLEAAGFKAAPKAARGVNFQLPNEDVRAKQDDDADGSEDSSDDDDSENSGD
EEEEKVTAESDSEEDDSSDDEEDDSSEEEFKRPEEPKRRSAEDNSSKNPASKKRKK
VTPQKIDSKKPHYHVATPHPSKQAGKNSGGGSTGETSKQQQTPKSAGAFGCKSCTRTF
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 123.4; DB 8; Length 885;
Pred. No. 4.4e-17;
0; Mismatches 276; Indels 0;
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                                        /organism-"Arabidopsis thaliana"
                                                                                                                                                                 /db_xref="G1:7804963"
                                                          /db_xref-"taxon:3702
                                                                                                                                                                                                                                                                                                    TSEMCLOSHTKAKHSAAA"
  Location/Qualifiers
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          /translation-"MEFWGVEVKNGKPLHLDPGLDRLVHISQVALGESKNNVTEPIOL
YTVOSSDKLLIGTLSHEKFFPQLSTETYLERNEASHTWYNGSVFFSOKTVDASDPEPE
DLIDDQLEAAGFKAAFKAARQDDDAGGSFEDSSDDDSENSG
EEEEKVTAESDSEEDDSSDEEDDSSEEETPKKPEEFKKSAEPDSSDDDSSNKAKF
VTPQKTDSKKRHVHAATPHPSKQAGRNSGGGSTGETSKQOOTPKSAGAFGCKSCTRTF
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                                                                                                                                                                   Score 124.2; DB 8; Length 1236;
Pred. No. 2.8e-17;
0; Mismatches 278; Indels 0;
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Baldwin,D.Adelphi., Briggs,S.P. and Crane,V.C. Maize histone deacetylases and their use Patent: US 628843-A 17 11-SEP-2001;
Location/Qualifiers
1. 1307
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/db_xref-"GI:13926268"
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1 (bases 1 to 885)
Dangl.M., Brosch.G., Haas,H., Loidl.P., Graessle,S. and Lusser,A.
Molecular characterization of type-2 histone deacetylases in higher
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Dandl.M., Haas.H., Loidl.P. and Lusser.A.
Direct Submission
Submitted (31-APR-2000) Microbiology, University of Innsbruck,
Fritz-Pregl-Str. 3, Innsbruck 6020, Austria
                                                                                                                                                                                                                                                                                                                             79 TCGTCGCAATGGAGTTCTGGGGTGAAGAGTGAAGCCAGGAGCCACGGTTTCTTGCAAAG 138
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Arabidopsis thaliana putative histone deacetylase HD2c mRNA,
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0; Mismatches 237; Indels
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                                                                                                                                               Query Match 13.2%;
Best Local Similarity 54.5%;
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                              Submitted (27-JAN-1998) Microbiology, Medical School, University of Innsbruck, Fritz-Pregl-Str. 3, Innsbruck 6020, Austria Location/Qualiflers
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YTVGGAKLVJGTLSQDKFPQISFDJYPDKEFELSHSGTKANVHFIGYKSPNIEQDDFT
SSDEDVPEAVPARAPTAVTNGNAGAAVVKADTKPRAKPFARFEKFESPEEDES
DDEDESEEDDDSEKGWYVBODGSDDDEEEDSEBEEETPKKFPPIKKRPNESVSKT
PVSGKKAKPAAAPASTPQKTEKKKGGHTATPHPAKKGCKSPVNANQSPKSGCQSSGGN
NNKKPPNSGKQFGSNNKGSNKGKKGGKRA"
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  PLN 11-FEB-1998
                                                                                                               thale cress.
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                   Dangl, M., Haas, H. and Loidl, P.
Arabidopsis thaliana complete cDNA-sequence homologous to Zea mays
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106, 1241-1255, 1994)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 gagaacatccctcagcttttctqtgatttggtattcqacaaggagtttgagctttctcac 288
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AF044914 918 bp mRNA linear PLN 11-FF
Arabidopsis thaliana putative histone deacetylase (HD2) mRNA,
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/product="putative histone deacetylase"
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Pred. No. 6.6e-23;
0; Mismatches 127;
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/cultivar-"Columbia"
/db_xref-"taxon:3702"
/clone-"133F1577"
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/db_xref="G1:2854070"
                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 918)
Dangl,M., Haas,H. and Loidl,P.
Direct Submission
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64.8%;
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Best Local Similarity
Matches 239; Conserv
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265 gacaaggagtttgagctttctcacacttggggaaaaggaagtgtttactttgttggatac 324
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Pred. No. 2.4e-24;
0; Mismatches 138;
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/db_xref="taxon:3702"
1 237 c 296 g 290 t
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                                                                                                                        385 gtteetgetgggaatgetgeeaaggetgtaget 417
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Seguence 7 from Patent EP1094112.
AX139020
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Best Local Similarity 64.1%;
Matches 252; Conservative (
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//product-putative histone deacetylase"
//protein_de=AAG28473.1"
//db_xref="401:11066137"
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DDEDESEEDDDSEKGMDVDEDDSDDDEEBDSEDEEEEFTPRKPEPEINEREDS
DPSDESEEDDDSEKGMDVDEDDSDDDEEBDSEDSEEEFTPRKPEPEINKRFPNRSVSKT
PWSGKRARAPAAAPASTPQKTEKKGGHTATPHPAKKGGKSPVNANOSPKSGGQSSGGN
NWKRPPNSGKOFGSNRKGSRGGRGRA"
234 C 288 9 288 L
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Arabidopsis thaliana putative histone deacetylase (HD2B) mRNA,
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Mukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                             1 (bases 1 to 1187)
W.K., Than,L., Mailk,K., Brown,D. and Miki,B.
Functional analysis of HD2 histone deacetylase homologs in
Arabidopsis thaliana
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/organism-"Arabidopsis thallana"
/cultivar-"Columbia"
/db_xref-"taxon:3702"
/clone-"133F15"
                              4 08 GCTGTTCCTGCTCTGCCCTACTGCTGTTACT 440
            gttootgetgggaatgetgceaaggetgtaget
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/codon_start-1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; endicotyledons; core eudicots;
Spermatophyta; Magnollophyta; endicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1218)
Wu.K., Miki, B.L., Tian, L. and Brown, D.C.
Repressing gene expression in plants
Patent: EP 1094112-A 7.5-Apr-2001;
The Minister of Agriculture and Agri-Food (CA)
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274 GATAAAGAGTTTGAGCTTTCACAGGGGTACCAAAGCAAATGTTCATTGGCTAC
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| Db 61414 TJ | TIGITATAGCTTTCTGTGATTTGTCTTTTTTTTACCATTTCAGAATAATGACTGAGG 61355 | JOURNAL | Submitted (22-OCT-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA |
|--|---|---|---|
| 61354 | AGAIGAGACATCTTTTTGAACAAAIGTIGGIGACGCATTCTTGTGTTATGATTCTTGCA 61295 | | C.Mail 101 Collegeboundance, alabasequence.scanlolu.edu RIKEN Genomic Sciences Center (GSC) members carried out the |
| Qy 490 -e Db 61294 GA | | | collection and clustering of RAFL COMA: 'RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K. |
| Qy 549 gc | gcctgcatcaagcaagaagagctaatgaaactacccctaaagcacctgtgtcagcaaa 608 | | The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAPL CDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., |
| Qy 609 98 - Db 61174 G | gaaggcgaaagtagcagttactcctcagaaa | | Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W. |
| 640 | | | Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSD/Stanford) contributed consilly to this work as placed. |
| Db 61114 A7 | ATTATTCACTAAATTGGGAAACACGAGTATTCATTTGAACCTGCATCGTCTTCTTTGGCA 61055 | FEATURES | |
| Qy 641 ce | cagatgagaagaagaaggggaaaggctgcaaaccagagcccaaagtcggccagtcaag 700 | | |
| Oy 701 to 11 Db 60994 TC | tetcatgtggttcatgcaagaa | auab | /clone="RAFL08-18-E14" /note="This clone is in pBluescript" 1172 /gene="Affs22650. MD722.7" |
| 723 | | CDS | 75995 /qene="At5q22650; MDJ22.7" |
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| Oy 786 az Db 60814 AJ | aagtggtttettattagagettgtgatttetatggaattttgeetgtagtetttatgaaa 845 | | SSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDES DDEDESEEDDDSEKGMYNEDDSDDDDFEEDSEDEEEETPKKPEPINKKRPNESVSKT PVSGKKAKPAAAPASTPOKTEEKKGGHTATPHPAKKGGKSPVNANGSPKSGGGSSGG NNNKKPPNSGKOFGGSNKGKGKKRA |
| 0y 846 co | | BASE COUNT ORIGIN | 362 a 234 c 285 g 291 t |
| 906 | 906 ggaqtetta 914 | Ouery Match Best Local Matches 25 | tch al Similarity 64.1%; Pred. No. 2.5e-24; 252; Conservative 0; Mismatches 138; Indels 3; Gaps 1; |
| RESULT 5 | GACICITA OUGGO | Qy 25 Db 51 | ttttctcaaccttgattcttagccatggagttctggggaattgaagttaaatcaggaaag 84 |
| AIUS9893 LOCUS DEFINITION | AY059893 1172 bp mRNA linear PLN 04-NOV-2001 Arabidopsis thaliana histone deacetylase-like protein (At5922650; MDJ22.7) mRNA, complete cds. | Qy 85 Db 111 | ccagttacagtgactcctgaagaagcattcttatccacgtttctcaggcatcgcttgga 144 |
| ACCESSION VERSION KEYWORDS SOURCE | AY059893 AY059893 GI:16649046 FLI_CDNA. thale cress. | 145 168 | |
| OKGANISA | Arabloopsis Lnailana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | Qy 205 Db 228 | ttggttctgggaactctatcgactgagaacatccctcagctttctgtgatttggtattc 264 |
| KEFERENCE AUTHORS | <pre>I (Dages I to 11/2) Nouyen, M. Xarlin Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Polcuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kanai, F., Kim</pre> | Qy 265 Db 288 | gacaaggagtttgagctttctcacacttggggaaaaggaagtgtttactttgttggatac 324 |
| TITLE | Adwal,J., Nim,C., Lin,J., Liu,S.X., Natusaka,M., Fnam,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission | Oy 325 Db 348 | aaaactcccaacattgagccacaaggctattctgaggaagaagaagaagaagaagaa 384 |

| Copy F14402. These ESTS are the 5' and 3' sequences, respectively, of clone TAP0138." /codon_start=1 /evidence=not_experimental /product="hypothetical protein" /product="hypothetical protein" /protein_id="AAB70027.1" /db_xref="G1:2392764" /translation="MGYBKFPWFURFECGYEEVLLITKLANAKHGGFLVVNG LSENLSREGGEVFLWFEGKRWFDKKLPLGGGAVSSHLHKFESSVUVNGFQVLDS GAESVERIFERHPYMALEFRANNQQLAASCINVLLSLITTLCOSLQDISIDDLGGTEQ | om repeat_region | misc_feature 9649 repeat_region | /note="direct tepeat 2, copy H" /rpt_type=direct misc_feature complement(26833. 29405) Ouery Match Best Local Similarity 61.8%; Pred. No. 4.6e-45; Matches 784; Conservative 0; Mismatches 0; Indels 485; Gaps | Qy 131 aggcatcgcttggagaatgtaaaaacaagaagggagaqttLgtgcctttacatgtaaag Db 61954 AGGCATCGCTTGCAGAATGTAAAACAAGAAGGAGAGTTTGTGCCTTTACATGTAAA Qy 191 ttgggaaccagaacttggttctggaactctatcgactgagaacatcctcagcttttc Db 61894 TTGGAACCAGAACTGTTCTGGGAAACACACAACAACATCCTCACCTTATTTTTTTT | Oy 251 gtgatttggtattcgacaaggagtttgagctttctcacacttggggaaaaggaagttt 310 | 0y 358 0y 358 0y 358 0y 358 | 0.9 385 Db 61594 0.9 394 0.9 61534 0.0 435 |
|---|---|---------------------------------------|--|---|--|--|---|
| similar to chromosome V (7873-8427), indirect repeat (co B, 8428-8440), direct repeat (copy B, 8441-8443). /hote-"Region: Putative transposon" /evidencc-not_experimental /860, .7872 /hote-"liverted repeat flanking putative transposon from position 7873 to 8427, copy A" /rpt_type-inverted /860, .8445 /hote-"These 586 nucleotides are 97.9% identical to a region of chromosome V clone MBK5 (AB005234), position | /note="Region: Similar to clone MBK5" complement(84288440) /note="liverted repeat flanking putative transposon from position 7873 to 8427, copy B" /rpt_type=inverted 84418443 /note="direct repeat flanking putative transposon from | rom m 97 | /rpt_typerdirect complement(90139156) /note="predicted by Grail" /evidence-not_experimental complement(94469741) /note="predicted by Grail" | rimental 9741) y MZEF; shows moderately weak simila rimental 9775) peat 1, copy B; copy A located from | /rpi_type=inverted 9789. 10041 /note="direct repeat 1, copy B; copy A located from 8872 to 9139" /rpi_type=direct complement(9819. 10293) | /complement(9819. 10054) /note="predicted by Grail" /note="redicted by Grail" /vidence=not_experimental 12951="13621" /note="region shares 90.3% identity to chromosome V BAC T21804 (Ar00721) from position 32026 to 32690 on the reverse strand" | Complemen(1452317066) Complemen(1452317066) /qene="T12N15.3" /force="gene encoding hypothetical protein similar to T32N15.4" /cvidence=not_experimental /cvidence=not_experimental /cvidence=not_foln(1452314849,1500615264,1558416038 1632516643,1670616771,1696917066)) /qene="T32N15.3" is most similar to hypothetical protein T32N15.4 (most nucleotide sequence differences are second or third position changes separated by 3 to 5 bases of |
| repeat_region misc_feature | repeat_region repeat_region | repeat_region repeat_region | exon | exon repeat_region | repeat_region exon | exon misc_feature | gene |

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Acabidopsis thallana BAC T32N15 from chromosome III near 54 cM Sequencing, analysis, and annotation were performed in collaboration with the CSHL/WU/ABI Arabidopsis Sequencing consortium. Information on physical mapping, YAC and BAC library construction, and a more detailed annotation of the seqence can be viewed at http://www.cshl.org/arabweb/. Gene prediction programs Grail and MZEF were used in the assembly of coding regions. In certain regions of the BAC these exons are not incorporated into a good model gene and are thus annotated as single exons. BAC T32N15 has been mapped to ofromosome III near 54 cM and marker m249. A graphical display of the annotation of T32N15 can be found at http://www.cshl.org/arabweb/T32N15-titlepage.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7559. 3750
Anote-"function-putative MITES; region is 96.9% identical to the nucleotide sequence of A. thaliana BAC T7N9, GenBank accession number AC000348; although GRAIL predicts an exon from position 3620 to 3759 and translation of this earn are in a manual programs fail to protein T7N9.14; gene-prediction programs fail to assemble this entire exon into an MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type=dispersed
6329. .6981
/note="function=minisatellite; 23 copies of a 28-bp tandem
                                                                                                                                 Submitted (21-APR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"amino-terminus is not likely to be encoded by BAC 1732M15; sequence is similar to many entries of A. thaliana genomic sequence, for example MX110, GenBank accession number AB005248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCDEAFEPNVTDLMIAVRNVQMLHLISSATEVISQCCKGGLPMFKNLLVLVFIGNTE
RVWKVFLPLLLEHSPNLTKLCLESLFLILQGLYHGTDEDEFDETHIPRSNKVNMLRII
OCGGTENELKHISHFLLKMECLQLVQVNFSETIVDSKKVQLTEDLMKLPSASSRLTMQ
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VKSLSIVYKYSADFDWFRTVALDTPNLVTLLYSTYARHRYRHCNLESLVNATLDLHFL
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//note="function-direct_repeat; cognate A of direct repeat
flanking putative transposon from position 7873 to 8427"
/rpt_type-direct
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/note="putative non-autonomous transposon; genomic
organization is: direct repeat (copy A, position
7857-7859), indirect repeat (copy A, 7860-7872), region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="gene encoding hypothetical protein; 5' region of T32N15.1 is not likely to be encoded by BAC T32N15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
join(<404. .1327,1413. .1559,1616. .1903)
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7857. .7859
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Harbor, NY 11724, USA
3 (bases 1 to 101371)
Parnell, L.D.
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                                                                                                        Direct Submission
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                                                                                     241 CAGCTITICTGTGATITGGTATITGGACAAGGGGTTTGAGCTTTCTCACACTTGGGGAAAA 300
                                                                                                                                                                                                                                                                              tetgaeggaatggatgaagatgattetgatggtgaggattetgaggaagaagageetaea 540
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                        Gaps
                                           cacgogtecgtaaaaatcetetetttteteaacettgattettageeatggagttetgg 60
                                                      601 tcagcaaagaaggcgaaagtagcagttactcctcagaaaacagatgagaagaaggg
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  Length 939;
                       Indels
100.0%; Score 939; DB 6; I
100.0%; Pred. No. 5.2e-197;
ive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 939; Conservative
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RESULT AF195545

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SEPEPTVKRASSKKRANETTPRAPVSAKKAKVAVTPQKTDEKKKGGKAANQSPKSASQV
SCGSCKKTFNSGNALESHNKAKHAAAK"
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   PLN 01-NOV-2000
                                                                                                                                                                                                                                                                                                                                                Submitted (18-OCT-1999) Eastern Cereal and Oilseed Research Centre,
                                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                     Agriculture and Agri-Food Canada, Ottawa, Ontario KIA 0C6, Canada
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               Arabidopsis thaliana putative histone deacetylase (HD2A) mRNA, complete cds.
AR195545.1 GI:11066134
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                                                                                                                                                                                                l (bases 1 to 914)
Wu,K., Tian,L., Malik,K., Brown,D. and Miki,B.
Functional analysis of HD2 histone deacetylase homologs
Arabidopsis thaliana
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Wu,K., Tlan,L., Malik,K., Brown,D. and Miki,B.
Direct Submission
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100.0%; Pred. No. 1.7e-191;
ive 0; Mismatches 0;
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/clone="211N2"
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Wu,K., Miki,B.L., Tlan,L. and Brown,D.C.
Repressing gene expression in plants
Patent: EP 1094112-A 5 25-APR-2001;
The Minister of Agriculture and Agri-Food (CA)
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2: /net/abss06/SIDS:

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4: __net_abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
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| te ca | AAZ97203 | 21 | 1024 | 5.8 | 54.6 | 45 |
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| DNA encoding novel | AAS90738 | 23 | 1072 | 5.8 | 54.8 | 44 |
| DNA encoding novel | AAS90729 | 23 | 801 | 5.8 | - | 43 |
| DNA encoding novel | AAS75452 | 23 | 372 | 5.8 | 54.8 | 42 |
| DNA encoding novel | AAS69688 | 23 | 1301 | 5.9 | 55 | 41 |
| Plasmodium falcipa | AAA70213 | 21 | 2658 | 6.0 | 5 | 40 |
| DNA encoding novel | AAS68926 | 23 | 291 | 6.0 | 56.4 | 39 |
| Murine LOBO homolo | AAZ23896 | 20 | 49999 | 6.0 | ٥. | 38 |
| gen | AAZ23891 | 20 | 49999 | 6.0 | | 37 |
| p160 | AAT89345 | 18 | 3901 | 6.0 | σ. | 36 |
| 60 CDNA | AAT89346 | 18 | 3211 | 6.0 | σ. | 35 |
| госу | AAT05868 | 17 | 3399 | 6.0 | 6 | 34 |
| Human nucleolin DN | AAC92553 | 22 | 2518 | 6.2 | 57.8 | <u>ω</u> |
| Human V3 loop HIV | AAV71745 | 20 | 2518 | 6.2 | 7 | 32 |
| s thall | AAC43629 | 21 | 520 | 6.3 | | 31 |
| ene. | AAT91872 | 18 | 3224 | 6.3 | 59 | 30 |
| 6 used | AAI01605 | 22 | 475 | 6.3 | 59 | 29 |
| #1666 | AAI32980 | 22 | 475 | 6.3 | 59 | 28 |
| #1613 | AAI11680 | 22 | 475 | 6.3 | 59 | 27 |
| bone n | AAK27085 | 22 | 475 | 6.3 | 59 | 26 |
| | AAK01642 | 22 | 475 | 6.3 | 59 | 25 |
| Probe #1619 for ge | ABA23153 | 22 | 475 | 6,3 | 59 | 24 |
| foetal | ABA53373 | 22 | 475 | 6.3 | 59 | 23 |
| | ABA42952 | 22 | 475 | 6.3 | 59 | 22 |
| Arabidopsis thalia | AAC39224 | 21 | 534 | 6.4 | 60 | 21 |
| Mouse ischaemic co | ABI99204 | 24 | 1260 | 6.4 | 60.4 | 20 |
| Arabidopsis thalia | AAC33860 | 21 | 895 | 6.5 | 61 | 19 |
| Mannose-1-phosphat | AAT91902 | 18 | 4000 | 6.6 | | 18 |
| | S | 23 | 2403 | 7.3 | 68.2 | 17 |
| melanc | ABL24559 | 23 | 303 | 7.3 | | 16 |
| | AAC37832 | 21 | 468 | 7.5 | 70 | 15 |
| | AAC34537 | 21 | 879 | 8.3 | 77.8 | 14 |
| dopsis tl | AAC49668 | 21 | 856 | 8.8 | 82.6 | 13 |
| histone | AAX90842 | 20 | 1283 | 10.5 | 98.4 | 12 |
| Maize histone deac | AAX90843 | 20 | 1191 | 10.6 | 100 | 11 |
| histone | AAX90844 | 20 | 1245 | 11.1 | 104.2 | 10 |

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ALIGNMENTS

AAF80352 ID AAF8

<u>,</u>

AAF80352;

AAF80352 standard; DNA; 939 BP.

Miki B, CA2316036-A1. Histone deacetylase; AtHDA2A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation; ds. Nucleotide sequence of a histone deacetylase designated AtHDA2A 24-AUG-2000; 2000CA-2316036 27-FEB-2001. Arabidopsis thaliana. 29-JUN-2001 (first entry) 27-AUG-1999; (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA Brown D, 99US-0383971. /product= "histone deacetylase AtHDA2A" Location/Qualifiers /*tag= Tian L, ž

Maize histone

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CC The present sequence encodes an Arabidopsis thaliana histone deacetylase CC designated AthDA2A. The protein is homologous to yeast RPD3 and HDA1. CC The polynucleotide sequence is used in the method of the invention. CC The specification describes a method for regulating gene expression in CC transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative CC eassociation with a gene of interest or with a nucleotide sequence CC encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, CC particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful CC as a functional test for identifying a phenotype associated with CC perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
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Pred. No. 9.2e-220;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Arabidopsis thaliana
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The present sequence encodes an Arabidopsis thaliana histone deacetylase designated AtHDA2B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histone deacetylase; AtHDA2B; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation; ds.
                                                                                                                                                                                                      347 aaatcccccaacatcgagcaggatgacttcactagttcggatgatgatgttcctgaa 406
               gaatgtaaaaacaagaagggagagtttgtgcctttacatgtaaaggttgggaaccagaac 204
                                                                       gacaaggagtttgagctttctcacacttggggaaaaggaagtgtttactttgttggatac
                                                                                                                                               gataaaagagtttgagctttcacacagcggtaccaaagcaaatgttcatttcattggctac
                                                        ttggttctgggaactctatcgactgagaacatccctcagcttttctgtgatttggtattc
                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of a histone deacetylase designated AtHDA2B.
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Pred. No. 1.5e-30;
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particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                              ttttctcaaccttgattcttagccatggagttctggggaattgaagttaaatcaggaaag 84
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                                                          Sequence 1212 BP; 393 A; 238 C; 293 G; 288 T; 0 other;
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                                                                                                                        Maize histone deacetylase; family 2, ZmHD2; chromatin structure; RNA polymerase I; ribosomal RNA production; promoter regulator; promoter; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for producing transgenic plants which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agggagagittgtgcctttacalgtaaaggttgggaaccagaacttggttctgggaactc 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.2%; Score 123.8; DB 20; Length 1307; 54.5%; Pred. No. 3.9e-22;
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                                                                                                                                                                                                                                                                                                  /product- "Maize histone deacetylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.9e-22;
0; Mismatches 237;
                                                                                                                                                                                                                                                    Location/Qualifiers
87..944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crane VC;
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                                                                                            Maize histone deacetylase-9 DNA.
В
                                                                                                                                                                                        disease response promoter; ds
AAX90845 standard; DNA; 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increased disease resistance
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Maize histone deacetylase; family 2, ZmHD2; chromatin structure; Mak polymerase I; ribosomal RNA production; promoter requiator; promoter; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for producing transgenic plants which have
                                                                                          281 tttctcacacttggggaaaaggaagtgtttactttgttggatacaaaactcccaacattg 340
                                                                                                                                                                        436 caatgcagaataatgaaattaaaatttctactgcaaaggttcccgtgaaggttggtatac 495
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                                                                                                                                                                                                                                         496 aaaatgctgatgaagatgaaacttctagtggtgatgatgatgatttcactgatagtgata 555
                                                                                                                                       ctgccaaggctgtagctaaaccaaaggcta-----agcctgcagaagtgaagccag 451
                                                                   341 agccacaaggctattctgaggaagaagaagaagaagaagaagaagttcctgctgqgaatg
                                316 tateacacaatteaaagacagetagtgtttettetgtggetacaagteaeetgtteete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 77-79; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize histone deacetylase-8 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX90844 standard; DNA; 1245 BP.
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disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
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                                                                                                                                                                                                                                                                   82 cgatggagttctggggtctcgaggtcaaacctggatccactgtcaagtgtgagcctggac 141
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                          316 acacatogaaaactaccagtgtatttttctctggttacaaggttgagcagccaattgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 atggetttateetgeaegttteeeaggetgeeettggggaateaaagaaaagtgaeagtg
                                                                                                                                                                                                                                                                                                                                                                                                             202 ccttaatg-----tatgtcaaagttgatgacaagaagcttgccattggaacgctctcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                227 ctgagaacatccctcagcttttctgtgatttggtattcgacaaggagtttgagctttctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 acacttggggaaaaggaagtgtttactttgttggatacaaaact----cccaacattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 agccacaaggctattctgaggaagaagaagaagaagaagaagaagttcctgctgggaatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 aggaaaatggcaaagctgatgggaaggaggagcagaaaaatcaagagaaggcagtagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize histone deacetylase; family 2, 2mHD2; chromatin structure;
                                                                                                                                                                                                  12;
                                                                                                                                                               Score 104.2; DB 20; Length 1245;
                                                                                                                                                                              Pred. No. 4.6e-17;
0; Mismatches 218; Indels
                                                                                                         Sequence 1245 BP; 385 A; 250 C; 324 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Maize histone deacetylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                           tch 11.1%;
al Similarity 53.7%;
267; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX90843 standard; DNA; 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 ctgaggaagaagagcet 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 ctgatgaggatgagtct 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..971
                                                                                                                                                           Query Match
Best Local Similarity
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The present sequence encodes a maize histone deacetylase . This DNA belongs to family 2, ZmHD2 and appears to affect chromatin structure at promoters of RNA polymerase I and thus regulate ribosomal RNA production. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                                                                                                         used for producing transgenic plants which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 atggagttctggggaattgaagttaaatcaggaaagccagttacagtgactcctgaagaa 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 atggagttctgggggtctcgaggtcaagcctggttccactgttaagtgtgagcctggatat 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acttggggaaaaggaagtgtttactttgttggataca----aaactcccaacattgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             goccaaggotgtagotaaaccaaaggotaagcotgcagaagtgaagccagotgttgatgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 gaagaggatgagtctgattc---tgacggaatggatgaagatgattctgatggtgaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccacaaggotattetgaggaagaagaagaagaagaagaagaagtteetgetgggaatget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 gaaaatggcaaagctgatgggaagaaacagaaaagtcaagaaaaggcagttgctgcacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1191 BP; 365 A; 242 C; 311 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.6%; Score 100; DB 20; 1
Best Local Similarity 54.9%; Pred. No. 5.5e-16;
Matches 268; Conservative 0; Mismatches 205;
                                                                                                                                                                                                                                                                                                          Claim 1; Page 73-75; 87pp; English.
                                                                                                                                                                         Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulated by histone deacetylase
                                                                                                                                                                                                                                                                          ncreased disease resistance
                                                                  99WO-US07370
                                                                                                    98US-0080563
                                                                                                                                     (PION-) PIONEER HI-BRED INT
                                                                                                                                                                       Briggs SP,
                                                                                                                                                                                                                                                         New deacetylase genes,
                                                                                                                                                                                                       WPI; 1999-611038/52
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                                                                                                                                                                                                                       P-PSDB; AAY28803
 W09951731-A2
                                                                02-APR-1999;
                                                                                                  03-APR-1998;
                                                                                                                                                                     Baldwin DA,
                                14-0CT-1999
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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16-APR-1999;
19-APR-1999;
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-MAY-1999;
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14-MAY-1999;
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                                                                                                                                                                                                                Maize histone deacetylase; family 2, ZmHD2; chromatin structure; RNA polymerase I; ribosomal RNA production; promoter regulator; promoter; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity; disease response promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a malze histone deacetylase. This DNA belongs to family 2, ZmiD2 and appears to affect chromatin structure at promoters of RNA polymerase I and thus regulate ribosomal RNA production. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for producing transgenic plants which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 atggagttctggggaattgaagttaaatcaggaaagccagttacagtgactcctgaagaa 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 atggagttctggggtctcgaggtcaagcctggttccactgttaagtgtgagcctggatat 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcattettateceaegttteteaggeategettggagaatgtaaaaaaeaagaagggagag 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggetttgtgetgeacettteecaggetgetettggggaateg-----aagaagagtgat 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 tttgtgcctttacatgtaaaggttgggaaccagaacttggttctgggaactctatcgact 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1283 BP; 383 A; 259 C; 333 G; 308 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product "Maize histone deacetylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 98.4; DB 20; 54.7%; Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 70-72; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulated by histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                          Maize histone deacetylase-6 DNA.
                                          AAX90842 standard; DNA; 1283 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increased disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0080563,
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                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deacetylase genes,
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Similarity 53.0%; Pred. No. 1.6e-11
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SUMMARIES

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| 28 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 38 | 40 | 41 | 42 | 43 | 44 | 4 5 |

ALIGNMENTS

| Sequence 17, Application US/09282305 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Crane, Virginia A. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses: TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses: TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses: TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses: CURRENT APPLICATION NUMBER: 1999/282,305 CURRENT APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1999-04-03 PRIOR FILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 17 LENGTH: 1307 TYPE: DNA ORGANISM: Zea mays FEATURE: NAME/KEY: CDS LOCATION: (87)(944) | Query Match 13.2%; Score 123.8; DB 4; Length 1307; Best Local Similarity 54.5%; Pred. No. 1e-24; Matches 298; Conservative 0; Mismatches 237; Indels 12; Gaps | 41 tcttagccatggagttctggggaattgaagttaaatcaggaaagccagttacagtgactc 100 | tegtegeaatggagttetggggtgaagaagtgaagecaggageeacggtttettgeaaag 138 | ctgaagaaggcattcttatccacgtttctcaggcatcgcttggagaatgtaaaaacaaga 160 | ttggtgatggtttggttatccaccittcacaggctgccctaggggaaccaaagaaag 195 | agggagagtttgtgcctttacatgtaaaggttgggaaccagaacttggttctgggaactc 220 | | | | ttteteacacttggggaaaaggaagtgtttactttgttggtacaaaacteccaacattg 340 | |
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INYENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-04-03
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Patent No. 6287843
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54.9%; Pred. No. 3.3e-18;
1ve 0; Mismatches 205; Indels 15;
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 13, Application US/09282305; Patent No. 6287843; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 54.99
Matches 268; Conservative
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US-09-282-305-13
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US-09-282-305-13
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                             477 tcaaaatcaagtccggattccaagaagagcaaggatgacgatgattctgatgaggacgag 536
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APPLICANT: Baldwin, Donald A.

APPLICANT: Baldwin, Donald A.

APPLICANT: Briggs, Steven P.

APPLICANT: Crans, Virginal C.

TILE REFERENCE: 5718-44,

CURRENT APPLICATION NUMBER: US/09/282,305

CURRENT APPLICATION NUMBER: 60/080,563

PRIOR FILING DATE: 1999-03-31

PRIOR FILING DATE: 1999-03-31

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                     Sequence 11, Application US/09282305 Patent No. 6287843
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; LOCATION: (79)..(996)
US-09-282-305-11
                                                                                          537 actgatga 544
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                                                                                                                                          RESULT 4
US-09-282-305-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                              GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               ....ONESSEE: __nunRESS:
...urkSSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
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REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
RESULT 5
US-08-202-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703)836-9300
TELEFA: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION. ANTISENSE MODULATION OF NUCLECLIN EXPRESSION
FILE REPERENCE: RTS-0109
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT APPLICATION NUMBER: US/09/433,699B
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
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Patent No. 596224
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                627 tactcctcaqaaaacagatgaqaagaagaaggqqqaaaggctgcaaac 675
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; LOCATION: (112)..(2235)
US-09-433-699-3
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; Sequence 8, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudl and Jack L. Strominger and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3211;
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                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
FILIG DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0%; Score 56.6; DB 2; Best Local Similarity 57.7%; Pred. No. 4.4e-06; Matches 101; Conservative 0; Mismatches 74;
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STREET: 60 State Street, Suite 510
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STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
                                             ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NUMBER OF SEQUENCES: 22
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EDNESS: single
                         CORRESPONDENCE ADDRESS:
                                                                                                                       Massachusetts
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                                                                                                                                                                  ZIP: 02109-1875
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                                                                                              Boston
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                                                                                                                                           COUNTRY:
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Patent No. 596224
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: p62 POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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6.0%; Score 56.6; DB 4;
Best Local Similarity 57.7%; Pred. No. 4.4e-06;
Matches 101; Conservative 0; Mismatches 74;
                                                         APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION NAMER: 08/574,959
FILING DATE: 40Andown>
FILING DATE: 40Andown>
ATTORNEY, AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REEECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEC ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 439..3157
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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FILING DATE: 19-DEC-95
ATTORNEYAGENT INFORMATION:
NAME: MANDERGRAGOURSE, ANY E.
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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STATE: Massachusetts
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3157 GAAGAAGAGGAAGAGGAGGAAGACTTTGAGGAAGAGGAAGAGAGATGATGATTTT 3216
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Patent No. 6291645
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamud1
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamud1
TITLE OF INVENTION: 50 POLYPEPTIDES, RELATED FOLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3901;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56.6; DB 2;
Pred. No. 4.9e-06;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: DFN-008
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                        DFN-008
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TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3901 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
                 REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
36,207
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                                                                                                                                                           LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.7%;
Matches 101; Conservative
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    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 439..3847
US-08-574-959A-6
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Patent No. 6158719
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, Mark
APPLICANT: Szebent, Atilia
TITLE OF INVENTION: METHODS FOR STABILIZATION AND
TITLE OF INVENTION: RETHORS FOR STABILIZATION OF PROTEINS B23
FILE REFERENCE: 13121.000202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 gattetgaeggaatggatgaaggatgattetgatggtgaggattetgaggaagaag 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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0
                                                                                                                                                                                                                                    Length 3901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 55.6; DB 4; Length 1164; 50.8%; Pred. No. 5.2e-06;
                                                                                                                                                                                                                                                                             74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                 Score 56.6; DB 4;
Pred. No. 4.9e-06;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/538,871
CURRENT FILING DATE: 2000-03-30
EARLIER APPLICATION NUMBER: 60/126,910
BARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                            LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          439..3847
                                                                                                                                                                                                                                 Ouery Match 6.0%;
Best Local Similarity 57.7%;
Matches 101; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                         CDS
                                                               MOLECULE TYPE: CDNA
                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 133; Conserv
                                                                                 FEATURE
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APPLICANT: Olson, Mark
APPLICANT: Olson, Mark
APPLICANT: Szebeni, Atilla
TITLE OF INVENTION: METHODS FOR STABILIZATION AND
TITLE OF INVENTION: METHODS FOR STABILIZATION AND
TITLE OF INVENTION: REMANDED FOR STABILIZATION AND
TITLE OF INVENTION: RUBBER: US/09/538,871
CURRENT APPLICATION NUMBER: US/09/538,871
CURRENT FILING DATE: 2000-03-30
RARLIER PELICATION NUMBER: 60/126,910
RARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 4
SOFWARE: FRELSER FREESER FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 gagtcagaagatgaagatgaggaagatgtaaaactcttaggcatgtctggaaagagtct 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 tggggaaaaggaagtgtttactttgttggaatacaaaactcccaacattgagccacaaggc 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of artificial sequence:/No. 6358718e - OTHER INFORMATION: synthetic construct
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Batent No. 5948676

GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: Chang, Vuan
APPLICANT: Russo, James J.
APPLICANT: Rediman, Isladore S.
APPLICANT: Rediman, Isladore S.
APPLICANT: Applicant Sarcoma Associated Herpesvirus, DNA
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 55.6; DB 4;
50.8%; Pred. No. 5.3e-06;
iive 0; Mismatches 129;
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                                                                                                                                                                             ; Sequence 1, Application US/09538871
; Patent No. 6358718
                                                 625 gaaactgaagaaaaggttccag 646
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532 gageetacacetaagaageetg
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Best Local Similarity 50.8%
Matches 133; Conservative
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LENGTH: 1232
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US-08-728-323A-1
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APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESYIRUS, DNA ENCODING SAME AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.6%; Score 52.2; DB 2; Length 3489; Best Local Similarity 55.9%; Pred. No. 7.5e-05; Matches 99; Conservative 0; Mismatches 78; Indels 0
                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/52268/JPW/MSC/SKS
TELEFROM_CONTENT INFORMATION:
TELEFRAX: 212-778-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
: 1185 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08770379
Patent No. 5849564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                      COMPUTER READABLE FORM:
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                                         New York
: U.S.A.
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                                                           COUNTRY:
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DD 20983 TGAGGAGGAGGAGGAGGATGACGAGGATGACGAGGATGACGA 20924
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Db 20923 GGAGGATGACGAGGAGGAGGATGACGAGGATGACGA 20864
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US-08-757-669A-20/c
; Sequence 20, Application US/08757669A
; Patent No. 6183751
; CENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: MORENION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; TITLE OF ENDENTES: 20
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.6%; Score 52.2; DB 2; Length 32207; Best Local Similarity 55.9%; Pred. No. 0.00021; Matches 99; Conservative 0; Mismatches 78; Indels 0;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTAME: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 52.42
REFERENCE/DOCKET NUMBER: 52.42
TELEPHONE: (212) 391.0525
INFORMATION FOR SED ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32.207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/757,669
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
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ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-08-770-379-20
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ö 0; Gaps Query Match 5.6%; Score 52.2; DB 4; Length 32207; Best Local Similarity 55.9%; Pred. No. 0.00021; Matches 99; Conservative 0; Mismatches 78; Indels 0; ò

Search completed: May 2, 2002, 20:15:18 Job time: 15105 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 15:42:36 ; Search time 3265.32 Seconds

(without alignments)

3881.286 Million cell updates/sec
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Title: US-09-645-337-5
Perfect score: 939
Sequence: 1 cacgcgtccgtaaaaatcct......aaaaaaaaaaggcggccgc 939

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Total number of hits satisfying chosen parameters: 27472414

13736207 seqs, 6748477542 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
4: em_estmu:*
4: em_estmu:*
5: em_estpu:*
6: em_estpl:*
7: em_estro:*
8: em_estpl:*
17: em_estro:*
10: gb_est:*
11: gb_gss:*
13: em_gss.hum:*
14: em_gss_lum:*
15: em_gss_lum:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_vrt:*

| | Description | AV544477 AV544477 | AI995198 701502609 | N37851 19078 Lambd | BE523968 M44A9STM | BE844690 AD01A07T7 | T45874 9137 Lambda | BF279194 GA_ED003 | AV551556 AV551556 | BG131117 EST464009 | BF275467 GAED002 | AV549937 AV549937 | BI130765 G110P49Y | BG445639 GA_Ea002 | BF278973 GA_ED003 | BF270691 GAED000 | C99809 C99809 YAC | BI786647 sai51f09. |
|-----------|-------------------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|--------------------|
| SUMMARIES | ΩI | AV544477 | A1995198 | N37851 | BE523968 | BE844690 | T45874 | BF279194 | AV551556 | BG131117 | BF275467 | AV549937 | BI130765 | BG445639 | BF278973 | BF270691 | 608660 | BI786647 |
| | 82 | 6 | 6 | 10 | 10 | 10 | 10 | 10 | 6 | 10 | 10 | σ | 10 | 10 | 10 | 10 | 10 | 10 |
| | % Query Match Length DB | 636 | 534 | 434 | 422 | 728 | 504 | 543 | 378 | 759 | 875 | 327 | 511 | 865 | 517 | 715 | 382 | 260 |
| | Query Match | 67.7 | 48.1 | 39.1 | 16.6 | 16.6 | 16.0 | 15.6 | 15.5 | 15.1 | 15.1 | 15.0 | 14.9 | 14.7 | 14.5 | 14.5 | 14.4 | 14.0 |
| | Score | 636 | 451.2 | 367.6 | 156.2 | 156.2 | 149.8 | 146.8 | 145.8 | 141.6 | 141.6 | 141 | 140.2 | 137.8 | 136.2 | 136 | 135.6 | 131.2 |
| | Result No. | c 1 | 7 | æ | 4 | Ŋ | ٥ | 7 | œ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 |

| BM177387 saj80q01. | AW906751 EST342874 | AW929159 EST337947 | BI924066 EST543955 | ç | AW615938 EST325304 | | BG134979 EST467871 | BE449829 EST361267 | B1934377 EST554266 | BI930352 EST550241 | BI924005 EST543894 | | BGS95734 EST494412 | AW429116 EST306572 | BE343018 EST395862 | BE343072 EST395916 | BF460278 073G03 Ma | BF187099 EST443386 | A1776222 EST257322 | | BE922565 EST426334 | | BI433232 EST535993 | AW039158 EST281393 | BG594317 EST492995 | BG889339 EST515190 | BG597002 EST495680 |
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| | 13.8 | 13.8 | | | | | • | 13.7 | 13.7 | 13.7 | 13.7 | 13.7 | | | | 13.6 | | | | | | | | | ω, | | 13.4 |
| 130.4 | 129.8 | 129.2 | 128.6 | 128.6 | 128.6 | 128.6 | 128.6 | 128.6 | 128.6 | 128.6 | 128.6 | 128.6 | 128 | 127.6 | 127.6 | 127.6 | 127.6 | 127 | 127 | 127 | 127 | 127 | 127 | 126.6 | 125.8 | 125.6 | 125.6 |
| 18 | 19 | 50 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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AV544477 Arabidopsis thaliana roots Columbia Arabidopsis thaliana CDNA clone R245c06F 3', mRNA sequence.
AV544477
AV544477
AV544477
BST. GI:8715891
                                                                                                                                                                                  Arabidopsis thaliana

Bukaryota; Lialiana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bogermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 636)

Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

DNA Res. 7, 175-180 (2000)

20363093

Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuékazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type-"roots"
/note-"Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Arabidopsis thaliana"
/strain-"Columbia"
/db_xratc_taxon:3702"
/clone-"RA45c06F"
/clone-lib-"Arabidopsis thaliana roots Columbia"
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67.7%; Score 636; DB 9; Length 636;

Query Match

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Chen,J., Moniyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guejfer,K., Kim,C., Doyle,M., Brzoska,P., Guejfer,B., Guejffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D.
Arabidopsis thallana Gene Expression MicroArray
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Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
                Indels
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Arabidopsis thaliana
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Arabidopsis thallana
Eukaryopsis Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Hrassicaceac; Arabidopsis.
                                                                                                                   /db_stref="texton:3702" /db_stref="texton:3702" /db_stref="texton:3702" /clone="701502609" /clone_lib="A. thaliana, Ohio State clone set." /note="coba library was made from selected clones from tarabidopsis thaliana Ohio State clone set."
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19078 Lambda-PRL2 Arabidopsis thallana cDNA clone 211N2T7, mRNA
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   St. Louis, MO 63134,
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Pred. No. 9.8e-77;
); Mismatches 3;
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/organism="Arabidopsis thallana"
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                                                     Email: service@genomesystems
                                                                    Location/Qualifiers
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4633 World Parkway Circle,
Tel: 877-577-2733
Fax: 314-427-3324
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98.18;
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/clone_lib="Lambda-PRL2"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_l: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and silqques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. " 17 others
,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant_Physiol. 106, 1241-1255 (1994)
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MSU-DOE Plant Research Laboratory
Michigan State University
MGU-DOE-PEL, Michigan State University, Plant Biology Bldg.,E.
Lansing,Mi
Tel: 517-353-0884
Fax: 517-353-9188
Exai: 517-353-9188
Exai: 22313tcn6jbm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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RESULT

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Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany 6
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142292916.
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Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                       EST 19-MAR-2001
                                                                                                                                                     thale cress.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                   1 (bases 1 to 422)
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
99 c 92 g 122 t
              W44A9STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M44A9 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 GCTACTAAGGTGACTCCTGAAGAAGACAGCCTTGTCCACATTTCTCAGGCTTCACTT--- 147
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/clone_lib-"Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col!"
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/organism="Arabidopsis thallana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
                                                                                                             BE523968.1 GI:9781946
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Benning, C
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145 gaatgtaaaaaacaagaagggagagtttgtgcctttacatgtaaaggttgggaaccagaac 204
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/tissue_type="mixed leaf and root"
/dev_stage="10-14 day old" / TOP10F."
/dev_stage="10-14 day old" / TOP10F."
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/note="Organ: whole seedlings; Vector: pT-Adv (CLONTECH); Site_1: EcoRI; Site_2: EcoRI; AD Arabidopsis thaliana library enriched for salt-induced transcripts from wildtype (Col-0 gil) 10-14 day-old seedlings treated with 160 mM Nacl for 4 hours."
                                                                                                                                                                        BE844690 728 bp mRNA linear EST 17-MAY-2001 AD01A0777 AD A. thaliana (Col-0 gll) library enriched for salt-induced transcripts; 10-14 day seedlings; 4h 160mM NaCl stress Arabidopsis thaliana CDNA clone AD01A07 similar to (AF044914) putative histone deacetylase, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes that are uniquely stress regulated in salt overly sensitive
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Matsumoto, T.K., Zhu, J., Cushman, J.C., Bressan, R.A. and Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 AAATCCCCCAACATCGAGCAGGATGACTTCACTAGTTCGGATGATGATGTTCCTGAA 387
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    728
    /organism-*Arabidopsis thallana"
    /strain-*ecotype Columbia g11"
    /db xref-*taxon:3702"
    /clone-*AD01A07"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (sos) mutants Plant Physiol. 126 (1), 363-375 (2001) 21249177
                                                            388 GCTGTTCCTGCTCCTGCCCTACTGCTGTTACT 420
                                      385 gttcctgctgggaatgctgccaaggctgtagct 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Blochemistry
University of Nevada
MS200, Reno, WN 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 728)
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Matches 252; Conservative
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POLYA-No.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; endicotyledons; core endicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 504)
Newman, T., deBrulin, F.J., Green, P., Keeqstra, K., Kende, H., McIntosh
Newman, T., deBrulin, F.J., Green, P., Keeqstra, K., Kende, H., McIntosh
E., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel
E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of annonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Lambda-PRI.2"
//clone_lib="Lambda-PRI.2"
//note="Vector: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
Lambda PRLZ is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T45874 1inear EST 09-JAN-1998 9137 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133F15T7, mRNA
324
                                                                                                                                                                                                                                                                                                                                                                                                            On Apr 14, 1993 this sequence version replaced g1:638462.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Hiology Bldg., E.
                                                                                                                                                                                                                                                                             205 ttggttctgggaactctatcgactgagaacatccctcagcttttctgtgatttggtattc
                                                                                                                                                               206 CITGITATIGGAACACTITCACAAGACAAGTICCCTCAGAITAGCTITGAITITGITITI
                                                                                                                                                                                                                                      265 gacaaggagtttgagctttctcacacttggggaaaaggaagtgtttactttgttggatac
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/strain-"var columbia"
/d_xref-"taxon:3702"
/clone-"133F15T7"
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Email: 22313tcn@ibm.ci.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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T45874.1 G1:934127
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SOURCE
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Enkaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eurosids II; Malvales; Malvaceae: Gossyptum.

1 (bases 1 to 543)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF279194 13near EST 07-MAR-2007 GA_Eb0037K03f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Eb0037K03f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="8400"
/db_xref="taxon:29729"
/db_xref="dA_Eb0037K03f"
/clone_lib="dGA_Eb0037K03f"
/clone_lib="dGSsyplum arboreum 7-10 dpa fiber library"
/tlssue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                          96 GCTACTAAGGTGACTCCTGAAGAAGACAGCCTTGTCCACATTTCTCAGGCTTCACTT--- 152
                                                                                                                                                                                                                                                                                                                                                                                  265 gacaaggagtttgagettteteacaettggggaaaaggaagtgtttaetttgttggatae 324
                                                                                                                                                                                                                                                                                                                                                                                                        384
                                                                                                                                                                                                                                145 gaatgtaaaaacaagaaagggaggagtttgtgcctttacatgtaaaggttgggaaccagaac 204
                                                                                                                                                                                                                                                                    153 GACTGCACAGTGAAATCTGGAGAATCTGTGGTTTTGAGTGTGACTGTTGGTGGGGGCTAAA 212
                                                                                                                                                                                                                                                                                                          205 ttggttctgggaactctatcgactgagaacatccctcagcttttctgtgatttggtattc 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 AAATCCCCCAACATCGAGCAGGATGACTTCACTAGTTCGGATGATGAGGATGTTCCTGAA 392
                                                                                                                                                      85 ccagitiacagigaciccigaagaaggcalicitalicacgillicicaggcalogciliga 144
                                        Gaps
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/note-"Vector: pBK-CMV; Site_1: EcoRI; Site_2: Xho!"
                                                                                              36 TTCTCTTCTTCCTCGTTCAACAACAATGGAGTTCTGGGGAGTTGCGGTGACAAAAAA 95
                                                                            25 ttttctcaaccttgattcttagccatggagttctggggaattgaagttaaatcaggaaag 84
                                                                                                                                                                                                                                                                                                                                213 CTGTTATTGGAACACTTTCACAAGACAAGTTCCCTCAGATTAGCTTTGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 aaaactcccaacattgagccacaaggctattctgaggaagaagaagaagaagaagaaga
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د د
  DB 10; Length 504;
Query Match 16.0%; Score 149.8; DB 10; Length
Best Local Similarity 64.6%; Pred. No. 5.3e-19;
Matches 239; Conservative 0; Mismatches 128; Indels
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: TAATACGACTCACTATAGGG
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Location/Qualifiers
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Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 GCTGTTCCTG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 gttcctgctg 394
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bopermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases II to 378)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation of I2,028 non-redundant expressed sequence tags from normalized and salze-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 bp mRNA linear EST 06-SEP-200
AV551556 Arabidopsis thallana roots Columbia Arabidopsis thallana
cDNA clone RZ128c12R 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 tggatacaaaactcccaacattgagccacaaggctattct.....gagga 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 CGCTTACAAAACTTTCATACCAGAGGAAGGTGATGATTTTGGTATGTCTAGCGAAGAAGA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 agaagaggaagaaggaagaagtteetgetggaatgetgecaaggetgtagetaaaee 422
                                                                                                                                                                                                                                                         78 aggaaagccagttacagtgactcctgaagaaggcattcttatccacgtttctcaggcatc 137
                                                                                                                                                                                                                                                                                                                                                                                        118 TGGACAGCCTATTAAAGCAGATCCTGGTGCTAACTACGTTATCCATCTTTCCCAGGCTTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 ccagaacttggttctgggaactctatcgactgagaacatccctcagcttttctgtgattt 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415 AAGCGAGGAGGAGGAGGAGGAGGAGCTTCCTGTTGCTGCTGCTGCTGCTGCAGTAAATGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                               138 gcttggagaatgtaaaaacaagaagggagagtttgtgcctttacatgtaaaggttgggaa 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 AAAAGCTAAGCCAGATGGAAAAACAGCCAAGGCTAATGCTGGGAAACCTGATGCTGTT 532
                                                                                                                                                                                                                         18 cctctctttttctcaaccttgattcttagccatggagttctggggaattgaagttaaatc
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                                                                                                                                                                     18;
                                                                                                              Length 543;
                                                                                                           Score 146.8; DB 10; Length
Pred. No. 2e-18;
0; Mismatches 172; Indels
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Kazusa DNA Research Institute
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     152
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/db_xref="taxon:3702"
/clone="R2128c12R"
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                                                                                                              15.6%;
60.3%;
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  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Hansen,C., Ronning,C., and Tanksley,S.
Generation of ESTs from tomato crown gall tissue
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I; Solanales, Solanneeae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="crown gails from full-grown plants (8 wks old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pBluescript SK(-); Sitc_1: EcoR1; Sitc_2: Xhol; Four wk old greenhouse plants were stab inoculated
                    Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 ccagttacagtgactcctgaagaaggcattcttatccacgttctcaggcatcgcttgga 144
                                                                                                                                                                                                                                                                                                                                 93 GCTACTAAGGTGACTCCTGAAGAAGACAGCCTTGTCCACATTCTCAGGCTTCACTT --- 149
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Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                         Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 aaaactcccaacattgagccacaaggctattctgaggaagaagaag 373
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                    SK-;
                                                                                                                                     Score 145.8; DB 9;
Pred. No. 3.4e-18;
0; Mismatches 117;
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                    /note-"Vector: pBluescriptII
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                         109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="crown gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4081"
/clone="cTOE2J5"
/tissue_type="roots"
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BG131117.1 GI:12631305
                                                                                                                                     15.5%;
65.6%;
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                                                         84 c
                                                                                                                                                                           Conservative
                                    Xho!"
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                                                                                                                                                                         229;
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on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Hurr,
Cornell U.). Galls were allowed to develop for another 4
Wks, when gall tissue was frozen in liquid nitrogen."
1 139 c 193 g 181 t
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                                                                                                                                                                                                                                                                                                  71 ttaaatcaggaaagccagttacagtgactcctgaagaaggcaticilatccacgtiicic 130
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                                                                                                                                                                                                                                                                                                                                                                                                                    132 AGGCATCTCTAGGTGAGTTGAAGGATAAATCAGAAAGTGCCTGCTTGTCAGTGAATA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 TTGATGGCAAGAACTTGTTCTTGGGACACTCAACTCAGAGAGGTGCCTCAACAGCAAT 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 ATGATGATTCTGATGAGGATATCCCCCTCACTTGCCAACAGTGGTAAACCTGACCTA 431
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                                                                                                                                      15.1%; Score 141.6; DB 10; Length 759; 53.3%; Pred. No. 1.8e-17; Live 0; Mismatches 284; Indels 54;
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1 (Dases I to 875)

2 (Mang.R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Mood,TC., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Contact: Wing RA

Contact: Wing RA

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing Gelemson.edu

Seq prince: TAATACGACTCACTATAGGG

High quality sequence stop: 630.

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/clone="GA_Eb0024C01f"
/clone=llb="GASSppium arboreum 7-10 dpa fiber library"
/clone_ltype="Fibers isolated from bolis harvested 7-10
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/strain-"AKA"
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Gossypium arboreum
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/strain-"Columbia"
/db_xref="taxon:3702"
/clone="Rz106a10R"
/clone="Rz106a10R"
/clone_lib-"Arabidopsis thaliana roots Columbia"
/tissue_type-"roots"
/note-"Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Kazusa DNA Research Institute
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       EST 31-DEC-2001
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyla; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighlales; Salicaceae; Populus.
                                                                                                                                                                                                         1 (bases 1 to 511)
Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen
T., Karlsson, J., Teerl, T., Gustafsson, P., Bahlerao, R., Jansson, S.
Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and
Lundeberg, J.
B1130765 511 bp mRNA linear EST 31-DEC-?
G110P49Y Populus cambium cDNA library Populus tremula x Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccatggagttctggggaattgaagttaaatcaggaaagccagttacagtgactcctgaag 106
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/db_xref="taxon:47664"
/clone_lib="Populus cambium"
/note="Grgan: cambium"
123 c 100 g 151 t
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                                                                                                                                                                                                                                                                                                                                                          Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Fat: 46 8 790 8287
Fax: 46 8 245452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 140.2; DB 10; Similarity 64.1%; Pred. No. 3.7e-17; 1; Conservative 0; Mismatches 118;
                                                                                                                  Populus tremula x Populus tremuloides.
Populus tremula x Populus tremuloides
                                          tremuloides cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rikerl@biochem.kth.se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                      Gene expression in Populus
                                                                           BI130765.1 GI:18014736
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                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Erlandsson R
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Gossypium arboreum.
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Wing, R. A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber of the cotton fiber Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GA_Ea0029401f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 TCTTTCATCATCATAAATGGAGTTCTGGGGTATTGAAGTTAAAGCTGGACAGCCTAT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%; Score 137.8; DB 10; Length 865; nilarity 53.1%; Pred. No. 9.1e-17; Conservative 0; Mismatches 293; Indels 6;
                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Gossypium arboreum"
                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
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170 c 254 g 18
                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 5
High quality sequence stop: 751
Location/Qualifiers
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Gossypium arboreum
                                                                                                                                                                                                                                                                                                                                                          Tel: 864 656 7288
Fax: 864 656 4293
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University
Clomson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                              BF278973 517 bp mRNA linear EST 07-MAR-2003 GA_Eb0036G18f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Eb0036G18f, mRNA sequence.
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kukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II: Malvales; Malvaceae; Gossypium.
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/clone-"GA_Eb0036G18f"
/clone_lib-"Gossypium arboreum 7-10 dpa fiber library"
/tissue_type-"Fibers isolated from bolls harvested 7-10
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                                                                  570 agctaatgaaactacccctaaagcacctgtgtcagcaaagaaggcgaaagtagcagttac 629
                                                                                                            613 TGAAGATGATGCCGAGGATGAAGATGCAGAGATGGCTGGGGAGTGAAGTTCAGATGAGGA 672
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                                                                                                                                                       630 teeteagaaaacagatgagaagaagaaagggggaaagg 667
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence start: 4
High quality sequence stop: 514.
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KEYWORDS
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1 (bases 1 to 715)
Wing, R.A., Frisch, D., Ya, Y., Main, D., Rambo, T., Simmons, J., Henry D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the corton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF270691 715 bp mRNA linear EST 07-MAR-200:
GA_Eb0009C15f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Eb0009C15f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Fibers isolated from boils harvested 7-10 dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain-"AKA"
/cullivar-"8400"
/db.xref-"taxon:29729"
/clone-"6A_Eb0009015f"
/clone-lib-"Gossypium arboreum 7-10 dpa fiber library"
                                                                                                                                                                     330 toccaacattgagccacaaggctattotgaggaagaagaagaagaagaagaagaagttoc 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 GGATGAGGAACTTCCTGTGGCTGCTGAAAACGGAAAAGCTAAGACAGATGCAAAAACGGC 443
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210 tctgggaactctatcgactgagaacatccctcagcttttctgtgatttggtattcgacaa
                                                                                                                                                                                                                                                                                                                                                                                                                              327 TTTTGTCCCAGAG --- GAAGGCTCTGATGAATTTGATAGTGAGGAAGAAGTAGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 tgctgggaatgctgccaaggctgtagctaaaccaaaggctaagcctgcagaagtgaagcc
                                                                                207 TCTCGGAACACTTTCCCACCAGAATTGCCCGCAATTGTGTTTTGATTTTAGTATTTGAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fax: 864 656 7288
Fax: 
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63.1%; Pred. No. 2.1e-16;
Live 0; Mismatches 130;
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Gossypium arboreum
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Best Local Similarity
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Search completed: May 2, 2002, 18:43:44 Job time: 10868 sec

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11. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8. Net/abss06/SIDS1/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
9. Net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
10. Net/abss06/SIDS1/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
11. Net/abss06/SIDS1/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
12. Net/abss06/SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1990.DAT:*
13. Net/abss06/SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1990.DAT:*
14. Net/abss06/SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
15. Net/abss06/SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
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18. Net/abss06/SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
19. Net/abss06/SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
20. Net/abss06/SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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Maize histone deac
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                                                                                                                                              2, 2002, 20:14:52 ; Search time 144.83 Seconds (without alignments) 187.897 Million cell updates/sec
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Arabidopsis thalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
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AAB67813
AAG31484
AAG310894
AAG26185
AAB67814
AAY28803
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length: 2000000000
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Match Length
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Maximum DB seq
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ALIGNMENTS

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 47121.
                  AAG38221 standard; Protein; 245 AA
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990S-0128714
990S-0129845.
990S-0130077.
                                                                                                                                                                                                                      99US-0123180.
99US-0123548.
99US-0125788.
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                                                                                                                                                                                                                                                                      99US-0127462
                                                       (first entry)
                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                     EP1033405-A2.
                                                                                                                                                                                                                     05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
119-APR-1999;
21-APR-1999;
                                                                                                                                                                                          25-FEB-2000;
                                                       18-OCT-2000
                                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                             25-FEB-1999
                                     AAG38221;
        AAG38221
RESULT
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| 0132048. | 32407. | 32485. | 32487. | 32863. | 34256. | 34219. | 34221. | 34370. | 34768. | 35124 | 35353, | 35629. | 36021. | 36782. | 37222. | 37528. | 37724 | 38094 | 38540. | 38847. | 39119. | 39402. | 39492. | 39454. | 39455. | 39450 | 39458. | 39459. | 39460. | 39462. | 39463. | 39750. | 39817. | 39899. | 40353. | 40695. | 40823. | 40991. | 41287. | 41642. | 42055 | 42390. | 42803. | 42920. | 43542 | 43624. | 44005. | 44085. | 44000. | 44331. | 44332. | 44333. | 44335. | 44350 |
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                                                                                                                                                                                                                                                    121 AVAKPKAKPAEVKPAVDDEEDESDSDGMDEDDSDGEDSEEEEPTPKKPASSKKRANETTP 180
                                                                                                                                                                                                                                                                                181 KAPVSAKKAKVAVTPQKTDEKKKGGKAANQSPKSASQVSCGSCKKTFNSGNALESHNKAK 240
                                                                                                                                                                                                                                                                                                                ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEVPAGNAAK 120
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a histone deacetylase designated AtHDA2A.
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                                                                                                                                                                              100.0%; Score 1279; DB 21; Length 245; 100.0%; Pred. No. 2.1e-107; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDA1; ethylene-responsive phenotype; hypocotyl elongation
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                                                                                                                                                                                                                                                                                                                                                                                           AAB67813 standard; Protein; 245 AA.
                                     99US-0160768.
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                                                                                                                                                                                                                                                             The present sequence represents Arabidopsis thaliana histone deacetylase designated AtHDAA. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                             Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENIPOLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEFVPAGNAAK 120
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99US-0138094
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                          termination sequence.
                                            Arabidopsis thaliana
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21-JUN-1999;
22-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                       99.6%; Score 1274; DB 21; 100.0%; Pred. No. 6.3e-107;
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990S-0155486.
990S-0155559.
990S-01565458.
990S-0156717.
990S-01571753.
990S-0157865.
990S-0158029.
990S-0158029.
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99US-0161992.
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Matches 244; Conservative
                                                                                                                       99us-01
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|haaa 244
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61 ENIPOLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYS---EEEEEEEEVPAGN 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1261.5;
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99US - 0151438
99US - 0151363
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98.48;
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990S-0161369-
990S-0161360-
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990S-0161920-
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01-SEP-1999;
10-SEP-1999;
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990S-0148565.
990S-0148684.
990S-0149368.
990S-0149175.
990S-0149426.
990S-0149723.
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990S-0147493.
990S-0147935.
990S-0148171.
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99US-0147303
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                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 30547
                                            AAG26185 standard; Protein; 305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S - 0.121825.
999US - 0.123180.
99US - 0.123180.
99US - 0.125788.
99US - 0.125788.
99US - 0.126746.2.
99US - 0.126785.
99US - 0.126785.
99US - 0.126786.
99US - 0.126786.
99US - 0.136714.
99US - 0.13486.
99US - 0.134218.
99US - 0.13428.
99US - 0.13428.
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99US - 0.13428.
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                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                                                                                   AAG26185;
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RESULT
AAG26185
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The present sequence represents Arabidopsis thaliana histone deacetylase designated AtHDA2B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for requlating the particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                       Histone deacetylase; AtHDA2B; RPD3; gene expression; transgenic plant;
 150 EDDSDG····EDS--EEEEPTPKKPAS-SKKRANETTPKAPVSAKKAKVAV-···TPQKTD 199
                        180 eddsdddeeedsedeeeetpkkpepinkkrpnesvsktpvsgkkakpaaapastpgkte 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGY-SEEEEEEEEVPA---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTIST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 mefwgvavtpknatkvtpeedslvhisgasl-dctvksgesvvlsvtvggaklvigtlsg 59
                                                                200 EKKKGGKA-------ANOSPKSASOVSCG-SCKKTFNSGNALESHNKAKH 241
                                                                                                                                                                                                              Amino acid sequence of a histone deacetylase designated AtHDA2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 305;
                                                                                                                                                                                                                                                    HDA1; ethylene-responsive phenotype; hypocotyl elongation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.4%; Score 594; DH 22; 50.7%; Pred. No. 1.8e-45;
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                                                                                                                                        AAB67814 standard; Protein; 305 AA.
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                                                                                                                                                                                      (first entry)
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Best Local Similarity 50.7%
Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGY-SEEEEEEEEFPPA---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GNAAKAV----AKPKAKPAEVKPAVD----DEEDESDSD-----GM--D 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 305;
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Pred. No. 1.5e-46;
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                        99US-0149930
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                                                           27 - AUG - 1999;
27 - AUG - 1999;
27 - AUG - 1999;
30 - AUG - 1999;
31 - AUG - 1999;
                                                                                                                       01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                       04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
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20-SEP-1999;
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13-0CT-19
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15;

ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPN1---EPQGYSEEEEEEEEEVPA-- 115

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belonging to family 2, ZmHD2. This enzyme responsible for removing acetyl modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DMA. The HD uncleotide sequence can be used for producing transgenic plants with increased disease resistance.

Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                                                                                                                                                                                                                                                      Maize histone deacetylase; HD; HD cDNA; family 2, ZmHD2; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wew deacetylase genes, used for producing transgenic plants which have
                                                                                                                         116 -----GNAAKAV----AKPKAKPAEVKPAVD----DEEDESDSD------GM--D 149
                                                                            120 avtangnagaavvkadtkpkakpaevkpaeekpesdeedesddedeseedddsekgmdvd 179
                                                                                                         150 EDDSDG---EDS--EEEEPTPKKPAS-SKKRANETTPKAPVSAKKAKVAV---TPQKTD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present sequence is maize histone deacetylase encoded by HD cDNA
                                                                                                                                                                      200 EK------KKGGKA---ANQSPKSASQVSCG-SCKKTFNSGNAL-ESHNKAKH 241
                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 79-80; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulated by histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                AAY28804 standard; protein; 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increased disease resistance
                                                                                                                                                                                                                                                                                                                                                                         Maize histone deacetylase-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease response promoter.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                               ----GEDSEEEPTPKKPASSKKRANETTPKAPVSAKKAKVAVTP-Q 196
                                                                                                                                                                                                                                179 glspdegdddssdeddtsdddeeetptpkkpeagkkrgaenalktplsdkkakvatppag 238
                                                                                                                                                                                                                                                                                      ---KGGKAAN-----QSPKSASQVSCGSCKKTFNSGNALESHNKA 239
                                                                         ------GNAAKAYAKPKAKPA---EVKPAVD-DEEDESDSDGMDEDDSD----- 154
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99US-0126264
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99US-0136021
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Gaps

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81; Indels

Matches 127; Conservative 29; Mismatches

Similarity

Query Match

Best Local

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40.1%; Score 513.5; DB 20; Length 311; 42.3%; Pred. No. 3.3e-38;

1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60

| 9US-0147799US-0147799US-014799US-014799US-014799US-014799US-014789US-014789US-014789US-014789US-014789 | 90x - 01x 80x - | 9998-01510 9998-01511 9998-01511 9998-01511 9998-01516 9998-0158-0158-0158-0158-0158-0158-0158-015 | 9908 - 01577 9908 - 01577 9908 - 01589 9008 - 01599 9008 - 01599 9008 - 01599 9008 - 01599 9008 - 01599 9008 - 01599 9008 - 01599 | 90x-01607 90x-01607 90x-01600 90x-01600 90x-01600 90x-01610 90x-01611 90x-01611 90x-01611 90x-01611 |
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| 990S-0136392. 990S-0136782. 990S-0137528. 990S-0137528. 990S-013754. 990S-0138094. | 990S-0139119. 990S-0139452. 990S-0139453. 990S-0139453. 990S-0139455. 990S-0139456. 990S-0139456. 990S-0139450. 990S-0139460. 990S-0139460. | 990S-0139763 990S-0139817. 990S-0139817. 990S-0140353. 990S-014069S. 990S-014069S. 990S-0141287. 990S-0141287. 990S-0141287. 990S-0142158. 990S-0142390. 990S-014290. | 99US-0143624. 99US-0144005. 99US-0144006. 99US-0144086. 99US-0144332. 99US-0144333. 99US-0144333. 99US-0144334. 99US-0144334. 99US-0144884. 99US-0144884. | 9905-0145085. 9905-0145087. 9905-0145089. 9905-0145145. 9905-0145218. 9905-0145218. 9905-0145218. 9905-0145913. 9905-0145919. 9905-0145919. 9905-0145951. |
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| 9US - 0147204 9US - 0147302 9US - 0147302 9US - 0147269 9US - 0147313 9US - 0147935 9US - 0148319 9US - 0148319 9US - 0148319 9US - 0148319 9US - 0148319 9US - 0148319 | 905-0149426 905-0149722 905-0149929 905-0149929 905-0150568 905-015068 905-0151066 905-0151066 905-0151080 905-0151303 905-0151303 905-0151303 905-0151303 905-0151303 905-0154018 905-0154018 | 9905-0156586 9905-0157517 9905-015753 9905-0157629 9905-0158232 9905-0158232 9905-0159293 9905-0159293 9905-0159330 9905-0159330 9905-0159331 9905-0159331 9905-0160914 9905-0160914 9905-0160914 9905-0160914 9905-0160914 9905-0160914 9905-0160914 9905-0160990 9905-0160990 9905-0161406 9905-0161406 9905-0161406 9905-0161406 9905-0161406 9905-0161406 9905-0161406 | 5661010-506 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize histone deacetylase; HD; HD cDNA; family 2, ZmHD2; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New deacetylase genes, used for producing transgenic plants which have
                                                                                                                                                            148 MDEDDSDGEDSEEEEPTPKKPASSKKRANETTPKAPVSAKKAKVAVTPQKTDEKKKGGKA 207
                                                                                                             Gaps
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                                                       Length 98
                                                                                                             Indels
                                            39.4%; Score 504; DE 2.1.
100.0%; Pred. No. 5.5e-38;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                    208 ANGSPKSASOVSCGSCKKTFNSGNALESHNKAKHAAAK 245
                                                                                                                                                                                                                                                                                                Claim 1; Page 76-77; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28803 standard; protein; 302 AA
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99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease response promoter.
                                                                              Best Local Similarity 100.
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Briggs SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-611038/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AA;
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29-OCT-1999;
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Maize histone deacetylase; HD; HD cDNA; family 2, ZmHD2; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is maize histone deacetylase encoded by HD cDNA belonging to family 2, ZmHD2. This enzyme responsible for removing acety modifications, may be localised to promofers targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New deacetylase genes, used for producing transgenic plants which have
                                                                                                                  196
                                                          154
                                                                         61 ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSE------EEEEEEEV
                                                                                                                    ---GEDSEEEFPTPKKPASSKKRANETTP-KAPVSAKKAKVAVTP--Q
                                                                                                                                              175 sseegdddssdeddtsddeeedtptpkkpevgkkraaessvlktplsdkkakva-tpssq
                                                        PA----GNA-----AKAVAKP-KAKPAEVKPAVDDEEDESDSDGMDEDDSD-----
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                                                                                                                                                                                                                                                                                                                                       AAY28802 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crane VC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                              Maize histone deacetylase-6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease resistance; toxin
disease response promoter
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                                                                                                                                                                                                                                    236 HNKAKH 241
                                                                                                                                                                                                                                                               294 hskakh 299
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DB 20; Length 305;

Score 487; DB 20 Pred. No. 8e-36;

38.1%;

Query Match Best Local Similarity

11;

Gaps

72;

1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60

Best Local Similarity 40.5 Matches 124; Conservative

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AAG15353 standard; Protein; 126 AA.
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99US-0132487.
99US-0132863.
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99US-0125788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
            285 AA;
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28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
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06-APR-1999;
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16-APR-1999,
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                                                                                                                                                                                                                                                                                                                                                                                              Maize histone deacetylase; HD; HD cDNA; family 2, ZmHD2; gene repression; eceryl modilication; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity; disease response promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New deacetylase genes, used for producing transgenic plants which have increased disease resistance -
                                                                          ENIPOLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSE------EEEEEEEFV 113
                                                                                                                      155 -------GEDSEEEPTPKKPASSKKRANETTP-KAPVSAKKAKVAVTP--Q 196
                                                                                                                                                                                          KTDEKK ------KGGKAAN ---- QSPKSA -- SQVSCGSCKKTFNSGNALESHN 237
                                                                                                       PA----GNA-----AKAVAKP-KAKPAEVKPAVDDEEDESDSDGMDEDDSD----- 154
 Gaps
                   1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60
                                 ,0,
 Indels
74;
37; Mismatches
                                                                                                                                                                                                                                                                                                             AAY28805 standard; protein; 285 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
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Conservative
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                                                                                                                                                                                                                                    238 KAKHAAAK 245
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Matches
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                                                                                                                                                                                                                                                                                     180 dsgseeqtptpkktevvvgkkraieaetp····sgkkakseqsaqktgdkvstshpakqs 235
                                                                                                                                                                                                                                                     ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTP----NIEPQGYSEEEEEREKKVPAG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                      120 nneikistakvpvkvgiqnadedetssgddddftdsdsemseedessdedevssdtdtsd 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 ---SEEEEPTPKKP--ASSKKRANET-TPKAPVSAKKAKVAVTPQKTDEK----KKG 204
                                                                   Gaps
                                                                                                                          1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60
                                                                                                                                                       54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 285;
                                                                                                                                                                                                                                                                                                                                                                         117 N-----AAKAVAK---PKAKPAEVKPAVDDEEDESDSDGMDEDDSDGED---
                                                                84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 GK------AANQSPKSASQVSCGSCKKTFNSGNALESHNKA-KHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SKQ ID NO: 15574.
Query Match 34.9%; Score 446; DB 20; Best Local Similarity 41.9%; Pred. No. 3.7e-32; Matches 122; Conservative 31; Mismatches 84;
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| 990S-0145218 990S-0145218 990S-0145218 990S-0145219 990S-0145919 990S-0145918 990S-0145918 990S-0145918 990S-0147302 990S-01471302 990S-01471302 990S-01471303 990S-01471303 990S-01471303 990S-01471303 990S-01471303 990S-01471303 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0159139 990S-0159139 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 990S-015929 |
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| 23 - Jul 1999; 23 - Jul 1999; 27 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 28 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Aug 1999; 30 - Aug 1999; 31 - Aug 1999; 32 - Aug 1999; 33 - Aug 1999; 34 - SEP - 1999; 35 - Aug 1999; 36 - Aug 1999; 37 - Aug 1999; 38 - Aug 1999; 39 - Aug 1999; 31 - Aug 1999; 32 - Aug 1999; 33 - Aug 1999; 34 - SEP - 1999; 35 - Aug 1999; 36 - Aug 1999; 37 - Aug 1999; 38 - Aug 1999; 39 - Aug 1999; 30 - Aug 1999; 31 - Aug 1999; 32 - SEP - 1999; 33 - Aug 1999; 34 - SEP - 1999; 35 - CCT - 1999; 36 - CCT - 1999; 37 - CCT - 1999; 38 - CCT - 1999; 39 - CCT - 1999; 31 - CCT - 1999; |
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                                                                                                    1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60
                                                                                                          Gaps
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                                                                                                                                                                                                                                         Query Match 29.3%; Score 374.5; DB 21; Length 208; Best Local Similarity 39.4%; Pred. No. 7e-26; Matches 86; Conservative 29; Mismatches 62; Indels 41; Gaps
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PR 21-0CT-1999; 99US-0160786.
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PR 25-0CT-1999; 99US-0161360.
PR 26-0CT-1999; 99US-0161360.
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OM protein - protein search, using sw model

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US-09-645-337-6 1279

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | æ | | | SOMMALES | | |
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| н | 513.5 | 40.1 | 311 | 4 | US-09-282-305-16 | Sequence 16, Appl | |
| 7 | 499 | 39.0 | 302 | 4 | US-09-282-305-14 | 14, | |
| e | 487 | 38.1 | 305 | 4 | US-09-282-305-12 | 12, | |
| 7 | 446 | 34.9 | 285 | 4 | US-09-282-305-18 | 18, | |
| 5 | 224 | 17.5 | | ~ | US-08-741-134-2 | 2, 8 | |
| 9 | 166.5 | 13.0 | 714 | 7 | US-08-990-114-3 | m | |
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| œ | 149 | 11.6 | 257 | 4 | US-09-538-871-4 | 4 | |
| 6 | 139.5 | 10.9 | | 7 | 741 | Sequence 6, Appli | |
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| 18 | 126.5 | 6.6 | 723 | 'n | PCT-US92-11107-11 | Sequence 11, Appl | |
| 19 | 121.5 | 9,5 | 240 | ~1 | US-08-114-555A-8 | Sequence 8, Appli | |
| 20 | | 9.5 | 240 | ٣ | US-08-559-397A-14 | Sequence 14, Appl | |
| 21 | 121.5 | 9.5 | 251 | 7 | US-08-766-738-3 | e, | |
| 22 | 121 | 5.5 | 542 | - | US-08-701-380-2 | Sequence 2, Appli | |
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RESULT 2 US-09-282-305-14

| 4 | Sequence 4, Appli | Sequence 2, Appli | Sequence 2, Appli | 7 | Sequence 1, Appli | 5, | 68, | Sequence 1, Appli | Sequence 28, Appl | Sequence 28, Appl | 28, | Sequence 26, Appl | Sequence 26, Appl | Sequence 26, Appl | 7, | 7 | Sequence 2, Appli |
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ALIGNMENTS

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| GENERAL Intromation:
| APPLICANT: Baldwin, Donald A.
| APPLICANT: Briggs, Steven P.
| APPLICANT: Cranc, Virginia C.
| TILE OF INVENTION: Malze Histone Deacctylases And Their Uses
| FILE REFERENCE: 5718-44,
| CURRENT FILING DATE: 1999-03-31
| PRIOR PLICATION NUMBER: 60/080,563
| PRIOR PLICATION NUMBER: 60/080,563
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: Patentin Ver. 2.0
                                                           APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
PRIOR TFLING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
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Sequence 14, Application US/09282305
Patent No. 6287843
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SOFTWARE: Patentin Ver. 2.0
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US-09-282-305-14
                                          GENERAL INFORMATION:
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                                       70; Gaps
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APPLICANT: Baldwin, Donald A.
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CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR FILING DATE: 1998-4-03
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 34.9%; Score 446; DB 4; Length 285; Best Local Similarity 41.9%; Pred. No. 1.2e-33; Matches 122; Conservative 31; Mismatches 84; Indels
38.1%; Score 487; DB 4; Length 305; 41.2%; Pred. No. 2.2e-37;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-----AAKAVAK---PKAKPAEVKPAVDDEEDESDSDGMDEDDSDGED-
                                   37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09282305
Patent No. 6287843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Ver. 2.0
                                   Matches 127; Conservative
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 KAKHAAAK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 | 1:
294 KANMGASE 301
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US-09-282-305-18
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SEQ ID NO 18
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RESULT 7
US-09-241-333-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 IPQLFCDLVFDKEFELSH-TWGKGSVYFVGYKTPNIEPQGYSERRBEBREF------VP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AKNKRKLENANDATANKKAKPDKKAGKNSAPAAESDSDDDDEDQLQKFLDGEDIDTDEND 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 -------DESDSDGMDED----DSDGEDSEEEEPTPKK----PASSKKRANETTPK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                               APPLICANT: Litwack, Gerald
APPLICANT: Alnemi, Emad And
APPLICANT: Fernandes-Alnemi, Teresa
TITLE OF INVENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 FWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLSTEN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FWGLIMEPNKRYTQVVEKP--FHISQAAM-DISTGDNDPCQVMVVVDGKNFLVCTLQKGK 58
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5861498ris
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
Query Match 17.5%; Score 224; DB 2; Length 412; Best Local Similarity 30.1%; Pred. No. 6.6e-13; Matches 82; Conservative 31; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AGNAAK -----AVAKPKAKP------AEVKPAVDDEE-
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IMMUNOPHILIN FKBP46 AND CC
TITLE OF INVENTION: AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 APVSAKKAKVAVTPQKTDEKKKGGKAANQSPK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: WordPerfect for Windows 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION ATTA:
APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: DELUCA, MATR
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-2090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3439
                                                                                                                                      Sequence 2, Application US/08741134 Patent No. 5861498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 412 amino acids
TYPE: amino acids
TOPLOGY: linear
MOLECULE TYPE: protein
US-08-741-134-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Litwac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19103
                                                                                            RESULT 5
US-08-741-134-2
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73 DKEFELSHTWGK-GSVYFVGYKTPNIEPQGYSEEEEEEEEFPAGNAAKAV----AKPKA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 KPAEVKPAV------DDEEDESDSDGMDEDDSDGEDSEEEFPTPKKPASSKKRANE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                    GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
ITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.0%; Score 166.5; DB 2; Best Local Similarity 33.8%; Pred. No. 2.8e-07; Matches 48; Conservative 20; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0451 US
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                    Sequence 3, Application US/08990114
Patent No. 5932475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 TTPKAPVSAKKAKV----AVTP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : ||| || || ||| : ||| 286 TKQKEVPEAKKQKVEGSESTIP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: 128842
                                                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: HE CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                   COUNTRY:
RESULT 6
US-08-990-114-3
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: WordPerfect for Windows 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,134
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APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 DEKKKGGKAANQSPKSASQV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 QESFKKQEKTPKTPKGPSSV 242
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-741-134-6
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 KPAEVKPAV------DDEEDESDSDGMDEDDSDGEDSEEEPTPKKPASSKKRANE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                               APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09538871
Patent No. 6358718
GENERAL INFORMATION:
APPLICANT: Olson, Mark
APPLICANT: Szebeni, Atilla
TITLE OF INVENTION: METHODS FOR STABILIZATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 13.0%; Score 166.5; DB 4 Local Similarity 33.8%; Pred. No. 2.8e-07; les 48; Conservative 20; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/990,114
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-865-0555
TELEFAX: 650-845-4166
Sequence 3, Application US/09241333 Patent No. 6313266 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 TTPKAPVSAKKAKV --- AVTP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 TKOKEVPEAKKOKVEGSESTTP 307
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
                                                                                                             APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1inear
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMEDIA:
LIBRARY: General Control of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-241-333-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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TITLE OF INVENTION: RENATURATION OF PROTEINS USING NUCLEOLAR PROTEINS H23
FILE REFERENCE: 13121.0002U2
CURRENT APPLICATION NUMBER: US/09/538,871
CURRENT FILING DATE: 2000-0-3-00
EARLIER APPLICATION NUMBER: 60/126,910
EARLIER PILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 GKGSVYFVGYKTPNIEPQGYSEEEEEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEEDE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SDSDGMDEDDSDGEDSEEEEPTPKKPASSKKRANET----TPKAPVSAKKAKVAVTPQKT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Litwack, Gerald
APPLICANT: Alnomri, Emad S.
APPLICANT: Alnomri, Emad S.
Typlicant: Ferrandoss-Alnomri, Teresa
Title OF INVENTION: IMMUNOPHILIN PKBP46 AND COMPOSITIONS FOR MAKING
TITLE OF INVENTION: AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of artificial sequence:/No. 6358718e; OTHER INFORMATION: synthetic construct
US-09-538-871-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5861498ris
STREET: One Liberty Place - 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 11.6%; Score 149; DB 4; Length 257; Best Local Similarity 27.9%; Pred. No. 3e-06; Matches 39; Conservative 26; Mismatches 69; Indels
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APPLICANT: Olson, Mark
APPLICANT: Seabeni, Atilla
APPLICANT: Seabeni, Atilla
TITLE OF INVENTION: METHODS FOR STABILIZATION AND
TITLE OF INVENTION: METHODS FOR STABILIZATION AND
TITLE OF INVENTION: METHODS POR STABILIZATION OF PROTEINS USING NUCLEOLAR PROTEINS B23
FILE REFERENCE: 13121.000202
CURRENT APPLICATION NUMBER: US/09/538,871
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: 60/126,910
EARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 EEEQKEEVRPEPKKSKKEKRRKHEEKEEEKRAKKVKVEFKKDLEEGPTKPKSKKEQDK- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEVPAGNAAKAVAKPKAKPAEVKPAVD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEEDESDSDCMDEDDSDCEDSEEEEPTPKKPASSKKRANET----TPKAPVSAKKAKVAV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                108 EEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEEDE----SDSDGMDEDDSDGEDSEEEF- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PTPKKPASSKKRANETTPKAPVSAKKAKVAVT-----PQKTDEKKKGGKA 207
                                                                                                                                                                                                                                                                                                                                                 51 QNLVLGTLSTENIPQLFCDLVFDKEFELSH-TWGKGSVYFVG--YKTPNIEPQGYSEEEE 107
                                                                                                                                                                                                                                                                                                                                                                                               118 QESVLLTLSPEAQYQQSLDLTITPEEEVQFIVTGSYAISLSGNYVKHPFDTPMGVEGEDE 177
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ): OTHER INFORMATION: Description of artificial sequence:/No. 6358718e - COTHER INFORMATION: synthelic construct US-09-538-871-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 IHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLSTENIPQLFCDLVFDKEFELSH--- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                Query Match
10.9%; Score 139.5; DB 2; Length 411;
Best Local Similarity 27.1%; Pred. No. 4.2e-05;
Matches 60; Conservative 22; Mismatches 98; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 ANGSPKSASQVSCGSCKKTFNSGNALESHN-----KAKHAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 --HKPKS-----KVLEGGIVIEDRTIGDGPQAKRGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.7%; Score 136.5; DB Best Local Similarity 25.4%; Pred. No. 5e-05; Matches 52; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09538871 Patent No. 6358718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                            9
                                                   SEQUENCE CHARACTERISTICS:
TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                          LENGTH: 411 amino acids TYPE: amino acid
                                                                                                                                               ; MOLECULE TYPE: protein US-08-741-134-6
                                                                                                                             linear
                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-538-871-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
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178 TIPKAPVSAKKAKVAVTPQKIDEKKKGGKAANQSPKSASQVSCGSCKKIFNS----- 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 EVKPAVDDEEDESDSDGMDEDDSDGEDSEEEEPTP--KKPASSKKRA------NE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 TTRPRRFSLIYSSESSLSDVSDSDRNKSTN--PHKIRRKAKNI-----SNNSQGKKSK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 TVTPEEGILIHVSQASLGEC----KNKKGEFVPLHVKVGNQNLVLGTLSTENIPQLFCDL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1085;
                                                                        APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 LIQRQIDNDDEGTESSDYQA -- VTDGEESENEEEESEEEED-----
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

SOFTWARE SPLICATION DATA: 05/08/11,080 FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.1%; Score 129.5; DB 1; Best Local Similarity 23.5%; Pred. No. 0.0013; Matches 62; Conservative 29; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                    STATE: P.C.
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
21P: 77210
ZIP: 7720ABLE FORM:
                                                                                                                                                                              E: Arnold, White & Durkee
P.O. Box 4433
              Sequence 28, Application US/08431080 Patent No. 5698686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- GNALESHNK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-431-080-28
US-08-431-080-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230
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Db 250 ALSFKFKKEDDGISFGNGNEGYNE 273

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APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: PO. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MSCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26.SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: ARCD:155/PAR TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                   COUNTRY: UNITED STATES OF AMERICA ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: SN 08/326,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
                   Sequence 28, Application US/08938534 Patent No. 5916752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: October 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEKAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                              Patent No. 5916752
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-938-534-28
US-08-938-534-28
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6 71 VFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEVPAGNAAKAVAKPKAKPA 130 ------DDEDDDDDDDDCSDSDSDSETSSDDENIDFVKLTAQRKKRAMKALSAMNTNSNT 191 178 TIPKAPVSAKKAKVAVIPQKIDEKKKGGKAANQSPKSASQVSCGSCKKIFNS----- 229 131 EVKPAVDDEEDESDSOGMDFDDSDGEDSEEEPTP--KKPASSKKRA-----NE 177 15 TVTPEEGILIHVSQASLGEC ---- KNKKGEFVPLHVKVGNQNLVLGTLSTENIPQLFCDL 70 47 TTRPRRFSLIYSSESSLSDVSDSDKNKSTN--PHKIKRKAKNI-----SNNSQGKKSK 97 Length 1085; Indels DB 2; 96 10.1%; Score 129.5; DB 23.5%; Pred. No. 0.0013; 29; Mismatches 230 -----CNALESHNK 238 Conservative Local Similarity 62; Query Match Matches g ò g ò g ò q ò

250 ALSFKFKKEDDGISFGNGNEGYNE 273

| RES | RESULT 13 |
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| 3 | Sequence 218, Application US/08961083 |
| | GENERAL INFORMATION: |
| | APPLICANT: Choi et. al. |
| ٠. | U2 |
| | NUMBER OF SEQUENCES: 452 |
| | CORRESPONDENCE ADDRESS: |
| | |
| | SITEET: 94IU Key West Avenue |
| | CITY: KOKVILLE |
| | SIATE: MAIL YIANG |
| | COUNTRY: USA |
| | COMPITTED PEADAUS FORM. |
| | MINISTER AMERICAN STORY TYPE: Diskette, 3.50 inch. 1.4Mb storage |
| | COMPUTER: HP Vectra 486/33 |
| | OPERATING SYSTEM: MSDOS version 6.2 |
| | SOFTWARE: ASCII Text |
| | |
| | APPLICATION NUMBER: US/08/961,083 |
| ٠. | FILING DATE: |
| | CLASSIFICATION: 435 |
| ٠. | PRIOR APPLICATION DATA: |
| | APPLICATION NUMBER: |
| ٠. | FILING DATE: |
| | ATTORNEY/AGENT INFORMATION: |
| | NAME: Brookes, A. Anders |
| | REGISTRATION NUMBER: 36,373 |
| | REFERENCE/DOCKET NUMBER: PB340P2 |
| | TELECOMMUNICATION INFORMATION: |
| | TELEPHONE: (301) 309-8504 |
| | TELEFAX: (301) 309-8512 |
| ٠. | INFORMATION FOR SEQ ID NO: 218: |
| ٠. | SEQUENCE CHARACTERISTICS: |
| ٠. | LENGTH: 565 amino acids |
| ٠. | TYPE: amino acid |
| | STRANDEDNESS: single |
| ٠. | ဌ |
| | ; MOLECULE TYPE: protein |
| 2 | 977-890-106-90 |

Ouery Match
9.9%; Score 127; DB 4; Length 565;
Best Local Similarity 30.3%; Pred. No. 0.00092;
Matches 43; Conservative 18; Mismatches 61; Indels 20; Gaps
Oy 90 VGYKTPNI---EPOGYSEEEEEEEEEVPAGNAAKAVAKPKAKP-AEVKPAVD------D 138

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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SOUTENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.

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98 EPQCYSEEEEEEEEVPAGNAAKAVAKPKAKP-AEVKPAVD-----DEEDESDSDGMD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 EDDSDGEDSEEEEPTPK-----KPASSKKRANETTPKAPVSAKKAKVAVTPQKTDEKK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 EVGGEVESKPEEKVAVKPESQPSDKPAEBESKVEQAGEPVAPREDEKA--PVEPEKQPEAP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
9.9%; Score 126.5; DB 4; Length 258;
Best Local Similarity 30.5%; Pred. No. 0.00036;
Matches 40; Conservative 17; Mismatches 57; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/07814964

Fatent No. 5359047

GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Bruhn, Steven
APPLICANT: Bruhn, Steven
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
Annapaceue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMNUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 258 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // MOLECULE TYPE: protein
US-08-961-083-90
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127 EEEKAVEETPK 137
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                                        : Maryland
RY: USA
20850
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                      Rockville
                                                                                                                                                                                                                                                             FILING DATE:
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US-07-814-964-11
                                      STATE: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :: | :| | : |: :|: || 402 IFSSIEKEEYAKLF-DYITQKKLHVSN-MGKDK---SGYKDVDFGDSDNENEPDAYLARL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 SEEEEEEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEED---ESDSDGMDED-----DS 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.9%; Score 126.5; DB 1; Length 723; 26.4%; Pred. No. 0.0014; tive 36; Mismatches 85; Indels 41.
                                                         COMPUTER: TADAPT GENERAL PLOS AND SECURATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENT Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 KAANQSPKSASQVSCGSCKKTFNSGNALESHNKAKHAAAK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: Domain
; LOCATION: 657..723
; OTHER INFORMATION: /label- Mixed Charge
US-07-814-964-11
                                                                                                                                                                                                                                                                                              NAME: Granahan, Patticia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: MIT-4787AAA
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 11
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 632.649
OTHER INFORMATION: /label= Basic II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IOMEGAISM: Drosophila SSRP (predicted)
CLONE: Drosophila SSRP (predicted)
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OTHER INFORMATION: /label= Basic 1
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LOCATION: 458..507
OTHER INFORMATION: /label= Acidic
FEATURE:
                                                Floppy disk
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Matches 58; Conservative
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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FEATURE:
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Search completed: May 2, 2002, 22:08:41 Job time: 6117 sec

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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1279
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Copyright (c) 1993 - 2000
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pir2:*
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pir4:*
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histone deacetylas
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| 132 | 132.5 | 133 | 133.5 | 134 | 134.5 | 134.5 | 135.5 | 136 | 136.5 | 136.5 | 136.5 | 137 | 138 | 138 | 138.5 |
| 10.3 | 10.4 | 10.4 | 10.4 | 10.5 | 10.5 | 10.5 | 10.6 | 10.6 | 10.7 | 10.7 | 10.7 | 10.7 | 10.8 | 10.8 | 10.8 |
| 374 | 971 | 532 | 1876 | 1320 | 325 | 280 | 557 | 651 | 723 | 611 | 292 | 590 | 705 | 699 | 971 |
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| C88734 | T24866 | T06029 | E97944 | JC5630 | T18283 | A61047 | A96527 | S18874 | A48217 | T06458 | A36089 | S63193 | S32644 | 138073 | T19431 |
| protein F32E10.6 { | hypothetical prote | hypothetical prote | zinc metalloprotei | TCOF1 protein - mo | hypothetical prote | ectodermal (ect) - | probable nuM1 prot | nucleolin - Africa | single-strand DNA/ | nucleolin homolog | nucleolar phosphop | hypothetical prote | nucleolin - Africa | nucleolar phosphop | hypothetical prote |

ALIGNMENTS

R;Dangl, M.; Haas, H.; Loidl, P. submitted to the EMBL Data Library, January 1998 A;Description: Arabidopsis thallana complete cDNA-sequence A;Reference number: Z26016 A;Accession: T52287 probable histone deacetylase (EC 3.5.1.-) [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T52287 histone deacetylase-like protein - Arabidopsis thaliana N;Alternate names: protein F17C15.160 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 RESULT T48401 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-305 <DAN> 뮍 Q Вþ Š Ъ Ş Ş A;Gene: HD2 C;Keywords: hydrolase 용 C; Genetics: A; Experimental source: cultivar Columbia A; Cross-references: EMBL: AF044914; PIDN: AAC02539.1 Matches 151; Query Match Best Local : 116 -----GNAAKAV-----AKPKAKPAEVKPAVD-----DEEDESDSD---------GM--D 200 180 240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSN 120 AVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVD 60 61 ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGY-SEEEEEEEEEEEVPA---- 115 1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVIGTLST 60 EK-----KKGGKA---ANQSPKSASQVSCG-SCKKTFNSGNAL-ESHNKAKH EDDSDG---EDS--EEEEPTPKKPAS-SKKRANETTPKAPVSAKKAKVAV----TPQKTD 199 DKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPN1EQDDFTSSDDEDVPEAVPAPAPT 119 EDDSDDDEEEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTE MEFWGVAVTPKNATKVTPEEDSLVHISQASL-DCTVKSGESVVLSVTVGGAKLVIGTLSQ Similarity Conservative 46.4%; Score 594; 50.7%; Pred. No. 6 26; Pred. No. 6.5e-31; 6; Mismatches 63 DB 2; 63; Length 305; Indels homologous to Zea mays HD2 58; Gaps 241 179 149 59 239 15;

990 44110 294 635 707 712 281 295 296 798 734 644 798 1881

151618 T10215 151116 A32915 T09648

nucleolar phosphop hypothetical prote NF-180 - sea lampr nucleophosmin - hu

nucleolin nucleophosmin - ch nucleolin - chicke

Chines

nucleolin - mouse nucleolin - human

nucleolin homolog

DNMS
A35804
JH0148
JC4295
S55395
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A24730
T33022
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D52858
D85135
D85135
S48647

nucleophosmin NO38 hypothetical prote nucleolus-cytoplas nucleolar protein

neurofilament prot nucleolar phosphop nucleophosmin - ra

heat-shock protein nucleolin - rat

neurofilament medi

hypothetical

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R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W submitted to the Protein Sequence Database, March 2000 A; Reference number: Z24492 A; Accession: T48401 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-296 <BEV> A; Cross-references: EMBL:AL162506 A; Experimental source: cultivar Columbia; BAC clone F17C15 C; Genetics: A:Map position: 5 A; Introns: 571; 28/3; 93/3; 116/3; 164/3; 195/3; 227/1 A:Note: F17C15 160
                                                                                                                                                                                                                                                R:Lusser, A.; Brosch, G.; Loidl, A.; Haas, H.; Loidl, Science 277, 88-91, 1997
Science 277, 88-91, 1997
A:Title: Identification of maize histone deacetylase i A:Reference number: Z15237; MUID:97349336
A:Recession: T04141
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-307 < LUS
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A;Experimental source: strain Cuzco 251
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                              histone descetylase (EC 3.5.1.-) HD2-p3
C;Species: Zes mays (maize)
C;Date: 23-Apr-1999 #sequence_revision
C;Accession: T04141
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                                                                                                                               Local Similarity
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       ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSE------EEEEEEEEEV 113
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                                         MEFWGLEVKPGSTVKCEPGYGFVLHLSQAALGE--SKKSDNALMYVKIDDQKLAIGTLSV 58
                                                                          MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60
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                                                                                                               Conservative
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39.5%;
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Pred. No. 7.4e-25;
1; Mismatches 81;
                                                                                                                             Score 482; DB 2; Pred. No. 8.6e-24;
                                                                                                                Mismatches
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FK506-binding 39k protein - fruit fly (Drosophila n C;Species: Drosophila melanogaster C;Date: 23-Jul-1995 *sequence_revision 03-Aug-1995 C;Accession: JC4090 R;Theopold, U.; Zotto, L.D.; Hultmark, D. Gene 156, 247-251, 1995
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fruit fly (Drosophila melanogaster)

#text_change

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Immunophilin FKBP46 - fall armyworm
C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 02-Sep-2000
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A55320
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C;Superfamily: yeast peptidy/prolyl isomerase FPR3; BKBI
C;Keywords: nucleus; phosphoprotein
C;Keywords: nucleus; phosphoprotein
F;324-371/Domain: BKBP-type peptidylprolyl isomerase hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-412 <ALN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 269, 30828-30834, 1994
A; Title: FKBP46, a novel Sf9 insect cell nuclear immunophilin that forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A55320
R; Alnemri, E.S.; Fei
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SVDMSKLSK----SQKRRLKKKLQQQAKQQPQ
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                                        APVSAKKAKVAVTPQKTDEKKKGGKAANQSPK
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                                                                                                                               DESDSDGMDED----DSDGEDSEEEEPTPKK----PASSKKRANETTPK 181
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30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleophosmin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1988 *sequence_revision 31-Dec-1988 *text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
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C;Keywords: molecular chaperone; nucleus
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F;269-316/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: yeast peptidylprolyl isomerase FPR3;
F;89-99/Region: acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-357 <THE>
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                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross:references: GB:X05496; NID:g64924; PIDN:CAA29046.1; PID:g64925
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-299 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 6, 1881-1890, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Schmidt-Zachmann, M.S.; Huegle-Doerr, B.; Franke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A29681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: fkbp39
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 KGGKAANQSPKSASQVSCGSCKKTFNSGNALESHNKAKHAAAK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VAKPKAKPA----EVKPAVDDEED------ESDSDGMD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 IPQVALDLNFSKGDRIMFYTAGDASVSLLGYL-----HDIDSEDDEDDDQMTIENLLNS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 IPQLFCDLVFDK-EFELSHTWGKGSVYFVGYKTPNIEPOGYSEEEEEEEEEVPAGNAAKA 121
                                                                                                                                                                                                                    83 GKGSVYFVGYKTPNIEPQGYSEEEEEEEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEEDE 142
                                                                                                                                                                                                                                                                                         Local Similarity
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KCKQDTKPQTPKTPKTPLSSEEIKAKMQTYLEKGNVLPKVEVKFANYVK--NCFRTEN
                                         AKK-----AKVAVTPQKTDEKK------KGGKAANQSPKSASQVSCGSCKKTFN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDDSDGEDSEEEEPTPKKP-----ASSKKRANETTPKAPVSAKKAKVAVTPQKTDEKK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAIKNSKKSEDDEDENESGEEDEEDTDDDSQIIEEYESFLENGEEEDDDDVDEDNEESGE 169
                                                                                                                                                                           GSGPVYVSGQHLVALEDLESSDDEDEEHEPSPK-NAKRIAPDSASKVPRKKTRLEEEEEED 165
                                                                                                                             SD-SDGMDEDDSDGEDSEEEEPTP-KKPASSKKRA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAKKEQPKAKEPAKQQPASKDPRTITGGVKIVDQVVGKGEEAK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDEQDSDDSEAEEEQPKRKVAKLSPGASAKKSGKEQNGVA----KKEEAKQQQKKKEKP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLSTEN 62
                                                                                    SDEDDDDDDDDDDDDEEEEEETPVKKTDSTKSKAAQKLNHNGKASALSTTQKTPKTPEQ 225
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                                                                                                                                                                                                                                                                  Conservative
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31.5%;
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                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                    Score 170.5;
Pred. No. 0.(
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                    0.00053;
                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                67;
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                                                                                                                                                                                                                                                                                                         Length 299;
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                                                                                                                                -NETTPKAPVS 185
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A; Residues: 1-694 < MAR2>
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A; Residues: 1-694 <MAR>
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                                                                                                                                                                                             Matches
                                                                                                                                                                                                                    Query Match
Best Local
                      211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chicken
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                             Conservative
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N;Alternate names: nucleolar protein C23
C;Speciles: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S08414; S10766; A32725; I50397; B30099
R;Maridor, G.; Nigg, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;267-275/Region: nuclear location signal
F;282-347/Domain: ribonucleoprotein repeat homology RRM1>
F;283-361/Domain: RNA binding #status predicted RNA1>
F;283-361/Domain: ribonucleoprotein repeat homology RRM2>
F;372-435/Domain: RNA binding #status predicted RNA2>
F;462-525/Domain: ribonucleoprotein repeat homology RRM3>
F;463-538/Domain: RNA binding #status predicted RNA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Keywords: DNA binding: duplication; nucleolus; nucleus; F:1-247/Domain: acidic <ACI>F:54-91/Region: 7-residue repeats (T-P-A-K-K-A-[A/V]) F:254-262/Region: nuclear location signal F:267-275/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 407-418, 'R', 420-519, 'T', 521-694 <BOR>
A; Residues: 407-418, 'R', 420-519, 'T', 521-694 <BOR>
A; Cross-references: GB; M21791; NID: g212411; PIDN. AAA48983.1; PID: g212412
C; Comment: Phosphorylation of this profesh by cdc2 kinase may contribute C; Comment: Phosphorylation of this profesh by cdc2 contribute C; Superfamily: nucleolin; ribonucleoprotein repeat homology
C; Superfamily: nucleolin; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Borer, R.A.; Lehner, C.F.; Eppenberger, H.M.; Nigg, Cell 56, 379-390, 199
A;Title: Major Nucleolar Proteins Shuttle between Nuclei A;Reference number: 150397; MUID:89119560
A;Accession: 150397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Peter, M.; Nakagawa, J.; Doree, M.; Labbe, J.C.; Nigg, E.A. Cell 60, 791-801, 1990
A;Title: Identification of major nucleolar proteins as candid A;Reference number: A32725; MUID:90182668
A;Accession: A32725
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Biochim. Biophys. Acta 1049, 126-133, 1990
A;Title: Structure and developmental express: A;Reference number: S10766; MUID:90304215
A;Accession: S10766
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A;Title: CDNA sequences of chicken nucleolin/C23 and A;Reference number: S08414; MUID:90206792
A;Accession: S08414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;56,63,70,77,85/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;554-618/Domain: ribonucleoprotein repeat homology <RRM4>
F;555-631/Domain: RNA binding #status predicted <RNA4>
F;632-694/Domain: glycine/arginine-rich <GRR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 56-62; 63-109; 197-214 <PET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translated from GB/EMBL/DDBJ
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PAKAKAESEDEEDEEDED-EDEEDEDDEEEDEEESEDEKPVKEAPGKRKKEMANKSAPEA
                                                                  PAEVKPAVDDEEDESDSDGMDEDDSDGEDSEEEEPTPKKPAS-----SKKRANETTPKA 182
                                                                                                                                                 KKSAAAVPAKKPAVVPAKQESEEEEEEDDEEEDDEEDDESEDEAMOTTPAPVKKPTPAKAT 210
                                                                                                                                                                                                                        KGSVYFVGYKTPNIEPQGYSEEEEEEEE....--EEVPAGNAAKAVAKP---KAK 128
                                                                                                                                                                                                                                                                                                                                          13.38;
33.98;
                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                  Score 170; DH 1; Length 694; Pred. No. 0.0013; 6; Mismatches 61; Indels
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RESULT
A27441
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A; Residues: 261-294 < 802>
A; Residues: 261-294 < 802>
A; Cross-references: 68:J03165; NID:g212454; PIDN:AAA48990.1;
C; Superfamily: nucleophosmin
C; Keywords: nucleus; phosphoprotein
F; 122-133/Region: glutamic acid-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ceil 56, 379-390, 1989
A;Title: Major Nucleolar Proteins Shuttle between Nucleus and Cytoplasm.
A:Reference number: I50397; MUID:89119560
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C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: $08415; $10767; $150398; $150399; A30099
R:Maridor, G.; Nigg, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:153-159/Region: nuclear location signal F:161-186/Region: aspartic acid/glutamic acid-rich F:161-186/Region: nuclear location signal F:190-197/Region: nuclear location signal F:127/Hinding site: phosphate (Ser) (covalent) #st.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X17200; NID:g63704; PIE R;Maridor, G.; Krek, W.; Nigg, E.A. Biochim. Biophys. Acta 1049, 126-133, 1990 A;Title: Structure and developmental expression A;Title: Structure and developmental expression
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A;Accession: I50399
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A; Residues: 1-97 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Borer, R.A.; Lehner, C.F.; Eppenberger, H.M.; Nigg, E.A Cell 56, 379-390, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-294 < MAR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S10766; MUID: 90304215
A; Accession: S10767
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A;Accession: S08415
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A;Title: cDNA sequences of chicken nucleolin/C23 and
       N; Alternate
                                 nucleolin -
                                                                                                                                                           골
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: prellminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-294 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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                                                                                                                                                         215 PS-TPASKTKTPDSKKDKSLTPKTPK
                                                                                                                                                                                                                                                                                                          134 PAV--DDEEDESDSDGMDEDDSDGEDSFFEEEPTP-KKPASSKKRANETTPKAPVSAKKAK 190
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                                                                                                                                                                                                        191 VAVTP----OKTDEKKKGGKAANQSPK 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                          76 FELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEEPPAGNAA--KAVAKPKAKPAEVK 133
                                                                                                                                                                                                                                                         PKLSEDDEDDDEDDDEDDDDDDEEEIKTPMKKPA--REPAGKNMQKAKQNGKDSK
                                                                                                                                                                                                                                                                                                                                                            FVLRLKCGSGPVYVSGQHLVALEEE----PESEDEEEDTKIGNASTKRPASGGGAKTPQKK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKKKTETPASAFSLFVKNLTPTKDYEELRTAIKEFFGKKNLQ----VSEVRIGSSKR 322
       names:
                                 Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
  nonchromosomal protein C23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
34.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 169;
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       nucleolar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 294
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       protein
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Query Match
Best Local Similarity
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A; Gene: xNopp180
C; Superfamily: no
C; Keywords: phos
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Nucleic Acids Res. 13, 5805-5816, 1985
A;Title: Cloning of cDNA encoding a 100 kDa nucleolar protein (nucleoline) of Chinese A;Reference number: A24070; MUID:85297777
A;Accession: A24070
A;Accession: A24070
A;Accession: A24070
A;Residues: 179-218 <LA3>
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
C;Keywords: DNA binding; nucleus; phosphoprotein
F;308-373/Domain: ribonucleoprotein repeat homology <RRM1>
F;394-455/Domain: ribonucleoprotein repeat homology <RRM3>
F;486-549/Domain: ribonucleoprotein repeat homology <RRM3>
F;572-636/Domain: ribonucleoprotein repeat homology <RRM4>
                                                                                                                                                                                                                                                                                                                                              nucleolar phosphoprotein - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999 C;Accession: I51618; S57757 R;Cairns, C.; McStay, B.
J. Cell Sci. 108, 3339-3347, 1995
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A:Recession: A24808
A:Molecule type: mRNA
A:Residues: 522-541, 'G', 543-544, 'R', 546-713 <LA2>
A:Cross-references: GB:M13757; NID:g191004; PIDN:AAA36961.1; PID:g387047
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: A27441; A24808; A24070
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Proc. Natl. Acad. Scl. U.S.A. 84, 147-1476, 1987
A; Title: Nucleolin, the major nucleolar protein o
A; Reference number: A27441; MUID:87175501
                                                                                                   C; Genetics
                                                                                                                                A; Cross-references:
                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1.990 <CAI>
                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                       A; Accession: 151618
                                                                                                                                                                                                                                                                                 A; Reference number:
                                                                                                                                                                                                                                                                                                                    A; Title: Identification and
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A; Residues: 1-713 <LAP>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 KPAEVKPAV-----DDEEDESDSDGMDEDDSDGEDSEEFEPTPKKPASSKKRANE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 DKEFELSHTWGK-GSYYFYGYKTPNIEPQGYSEEEEEEEEEVPAGNAAKAV----AKPKA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTPKAPVSAKKAKV ---- AVTP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APAKVVPVKAKNVAEEDDDDEEEDEDEEEEEEEEEEEEEEEEEEEEEEPVKPAPGKRKKEM 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDEFEPPVVKGKQGKVAAAAPASEDEDEEEDEEEEEEDEEEEDDSEEEEAMEITPAKGKK 224
   phosphoprotein
                                nucleolus-cytoplasm shuttle phosphoprotei
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                                                                                                                                EMBL: X88927;
                                                                                                                                                                                                                                                                                       151618; MUID: 96019267
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                                                                                                                                                                                                                                                                                                                    cDNA cloning of a Xenopus
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                                                                                                                                NID: 9895920; PIDN: CAA61368.1; PID: 9895921
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Pred. No. 0.
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Score Pred.

165. No.

.5; DB 0.0037;

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Length

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NF-180 - sea lamprey
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51116
R;Jacobs, A.J.; Kamholz, J.; Selzer, M.E.
                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL079350; GSPDB:GN00062; ATSP:T30C3.20 A;Experimental source: cultivar Columbia; BAC clone T30C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Bevan, M.; Rose, M.; Hempel, S.; Entlan, K.D.; Bancroft, submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T30C3.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
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A; Residues: 1-487 <BEV>
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A; Accession: T10215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SESSDSEDEKOGGKNTSTTKIANSTPKAAA----AECSEESSSS---EDEGKANGTSGK
                                                                                                                                                                                                            EQDDCQESANKSK
                                                                                                                                                                                                                                                     NSGNALESHNKAK
                                                                                                                                                                                                                                                                                              KQIVAIEGAHVPVLESEDEDEDGLPIPKGKSSEVENASGEKMVVDNDEQGSNKKRKAKAA 263
                                                                                                                                                                                                                                                                                                                                                                                      QLDEFEDFLDSNLERYRNAAAPKSGVIIEEIEDEEKPAKDNK-AKQTKKKSQASEGENAK
                                                                                                                                                                                                                                                                                                                                                                                                                        ------PTPK------KPASSKKRANETTPKAPVS----AK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEEDESDSDGMD-----EDDSDGEDSEEEE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNQ-NLVLGTLSTENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGFWGSDFVLLTYAGLEVKPGKPQAYNPKNEQG-KIHVTQATLGTGLSKEKSVI--QCSI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDVKQGAKAAKPTPKKAASSSSEDSSSDEDVSKAKKTNTAVSKSPVTTPKAVPAAKKESS 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEEEEEEEEVPAGN--AAKAVAKPKAKPAEVKPAVDDEEDESDSDGMDEDDSD-----
                                                                                                                                                                                                                                                                                                                                           KAKVAV-----TPQKTDEKKKG-----GKAANQSPKSASQV-----SCGSCK----KTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDKAPIALCSLLPNKIECCPLNLEFDDDDE------PVEFTVTGDRSIHLSGFLEYYQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GEDSEEEEPTPKKPASSK-------KRANE-----TTPKAPVSAKKAKV 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSEEEGKSKOPTGKSPAAKATAPPKKNPVAVNKDKPSSSSSSDSSGDDEKQKPKQAAAA 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 164; DB 2; Length 487; Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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د:
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C:Species: Homo sapiens (man)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: A33423; A32915; A30137; S06926; B26080; A26080
R:Zhang, X.T.; Thomis, D.C.; Samuel, C.E.
Blochem. Blophys. Res. Commun. 164, 176-184, 1989
A:Title: Isolation and characterization of a molecular cDNA clone of a human A; Reference number: A33423; MUID:90026373
A; Accession: A33423
A; Experimental source: clone hL6T R; Chan, P.K.; Chan, W.Y.; Yung, B.Y.M.; Cook, R.G.; Aldrich, J. Biol. Chem. 261, 14335-14341, 1986
A; Title: Amino acid sequence of a specific antigenic peptide A; Reference number: A92562; MUID:87033628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M28699; NID:g557545; PIDN:AAA58386.1; PID:g557546
R;Chan, W.Y.; Liu, Q.R.; Borjigin, J.; Busch, H.; Rennert, O.M.; Tease, L.A.; Chan, Biochemistry 28, 103-1039, 1989
Biochemistry 28, 103-1039, 1989
A;Tille: Characterization of the cDNA encoding human nucleophosmin and studies of it A;Reference number: A30137; MUID:89229105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Li, X.; McNeilage, L.J.; Whittingham, S. Biochem. Biophys. Res. Commun. 163, 72-78, 1 A;Title: The nucleotide sequence of a human A; Reference number: A32915; MUID:89374300 A; Accession: A32915
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A; Residues: 1-1110 < JAC>
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A;Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation
A;Reference number: 151116; MUID:95287814
                                                                                                                                               A;Molecule type: mRNA
A;Residues: 15-294 <HAL>
A;Cross-references: EMBL:X16934; NID:g32029; PIDN:CAA34809.1; PID:g825671
                                                                                                                                                                                                                                                                            A;Title: Nucleotide sequence of a cDNA clone A;Reference number: S06926; MUID:90098787 A;Accession: S06926
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M23613; NID:g189271; PIDN:AAA36380.1; PID:g189272 R;Hale, T.K.; Mansfield, B.C. Nucleic Acids Res. 17, 10112, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-294 < ZHA>
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A; Residues: 1-294 < CHAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A30137
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A; Residues: 1-294 <LIX>
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Best Local Similarity
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Pred. No. 0.014;
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                               of protein B23
                                                                                         M.B.; Ru, D.; Goldknopf,
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A;Title: Developmental and cell cycle regulation of Alfalfa nucMs1 a plant homolog of th A;Reference number: Z16796; MUID:96361876
A;Accession: T09648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09648
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C:Superfamily: nucleophosmin
C:Keywords: nucleolus; nucleus; phosphoprotein
F:120-132/Region: qlutamic acid-rich
F:152-158/Region: nuclear location signal
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A;Remiduem: 'P',214-215,'S',217-218,'SSS',222-294 <CHA2>
A;Crommon referencem: GB:J02590; NID:g190237; PIDN:AAA36473.1;
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A; Status: not common
                                                                                                                                                                                                                                                                                                                          A;Gene: nuMl
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-635 < BOE>
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N;Alternate names: nuMl protein
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A; Residues: 'P', 214-226 <CHAl>
                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X88845; NID:g1279562; PIDN:CAA61298.1; PID:g1279563
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                                                                                                                                                                                                                               Best
                                                                                                                                                                                                       Matches
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                                                 151 DDSDGEDSEEEEPTPKKPASSKKRANETTPKAPVSAKKAKV-----AVTPQ 196
                                                                                                                                                   105 REEEEEEEVPAGNAAKAVAKPKAKPAEVKPAVDUEEDESDSDG------
281 SDSDDEDDDSSSDEDKKPVASKKEVSESESDSSDDDHKMNIDKDSSDSDESEEESEDEPL 340
                                                                                                     221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 KAKVAVTPQ-KTDEKKKGGKAANQSPKSASQV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 ADEDDDDDDEEDDDDDDDDDDDDEEAEEKAPVKKSIRDTPAKNAQKSNQ------NGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 PAVDDEEDESDSDGMDEDDSDGEDSEEEEPTPKK-----PASSKKRANETTPKAPVSAK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 DSKPSSTPRSKGQESFKKQEKTPKTPKGPSSV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 GSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGKRSAPGGG-----SKVPQKKVKLA 159
                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 28.3%; Pred. No. 0.0051;
                                                                                                  ESSDEEDKKPAAKASKNVSAPTKKAASSSDEESDEESDEDEDAKPVSKPAAVAKKSKKDS 280
                                                                                                                                                                                                       47;
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28.5%;
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                                                                                                                                                                                                                               Pred. No. 0.014;
                                                                                                                                                                                                                                                    Score 153.5;
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A; Cross-references: GB: W22089; NID: 9200111; PIDN: AAA39841.1; PID: 9554246 C; Comment: This housekeeping protein is involved in the synthesis, packaging, C; Genetics: A; Introns: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; C; Superfamily: nucleolin; ribonucleoprotein repeat homology
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                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A29958; A40769; A56240; I84688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: nucleolin; ribonucleoprotein repeat homology C; Keywords: DNA binding; duplication; nucleus; phosphoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and structure of the nucleolin promoter A;Reference number: I48118; MUID:89121496 A;Accession: I84688
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A:Title: Structure of the mouse nucleolin gene.
A:Reference number: A29958; MUID:88316930
A:Accession: A29958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;396-458/Domain: ribonucleoprotein repeat homology <RRM2>
F;397-402/Region: RNA-binding RNP2 motif
F;431-438/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;311-316/Region: RNA-binding RNP2 motif F;349-356/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-44 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A56240; MUID:94344117
A;Accession: A56240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Yang, T.H.; Tsai, W.H.; Lee, Y.M.; Mol. Cell. Biol. 14, 6068-6074, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;488-551/Domain: ribonucleoprotein repeat homology <RRM3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F; 310-375/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Bourbon, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 2-19;558-567 < YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 2-20, 'X', 22-24 < PAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleolin -
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;607-614/Region:
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108 GKKGAAQAKALVPTPGKKGAATPAKGAKNGKNAKKEDSDEDEDEEDEDDSDEDEDDEEED 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 KTDEKK-----
                                               36 NKKG-----EFVPLHVKVGNQNLVLGTLSTENIPQLFCDLVFDKEFELSHTWGKGSVYFV 90
                                                                                                           48
                                                                                                                                                             6 IEVKSCKPVTVTPEEGILI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73-84, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; translated from GB/EMBL/DDBJ
                                                                                                     IPOKKGKKATTTPAKKVVVSQTKKAAVPTPAKKAAVTPGKKAVATPAKKNITPAKVIPTP 107
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                    RNA-binding RNP2 motif RNA-binding RNP1 motif
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                                                                                                                                                                                                                                                                                                                                                                                                          ribonucleoprotein repeat
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                                                                                                                                                                                                                                         12.0%;
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                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                      Score 153.5; DB Pred. No. 0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.; Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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1279
1 MEFWGIEVKSGKPVTVTPEE.....TFNSGNALESHNKAKHAAAK 245 105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 105224

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 3.3 | 32 | 31 | 30 | 29 | | | | 25 | | | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | | 11 | | Ī | 80 | • | 6 | ري ري | • | ω | 2 | _ | 20. | , . | • |
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| 125.5 | 126 | 126 | 126 | 126 | 126.5 | Ń | 128 | 128 | 128.5 | 129.5 | 130 | 131.5 | 136 | 137 | 138 | 139.5 | 144 | 145.5 | 149 | 149.5 | 150.5 | 151.5 | u | 153.5 | 153.5 | 155 | 166.5 | 169 | 170 | 170.5 | 191.5 | 224 | score | • | |
| 9. | 9.9 | 9.9 | | | 9.9 | | 10.0 | 10.0 | 10.0 | 10.1 | 10.2 | 10.3 | 10.6 | 10.7 | 10.8 | 10.9 | 11.3 | 11.4 | 11.6 | 11.7 | 11.8 | 11.8 | 12.0 | | 12.0 | ٠ | | 13.2 | 13.3 | 13.3 | 15.0 | 17.5 | Maten I | | de |
| 200 | 918 | 450 | 226 | 217 | 723 | 361 | 891 | 639 | 1411 | 1085 | 1982 | 731 | 650 | 590 | 699 | 411 | 292 | 704 | 292 | 644 | 281 | 712 | 706 | 706 | 411 | 294 | 713 | 294 | 694 | 299 | 357 | 412 | Length | | |
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| P05221 xenopus lae | | P13627 paracoccus | | | | | - | | | P39520 saccharomyc | drosophila | | 7 | | | | - | | | | | | æ | ٠, | | u | mesocr | 9 gallus | gallus q | | a. | 86 spo | Description | • | |

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| 1 ORC2_DROME 1 NFM_BOVIN 1 NFM_BOVIN 1 NFM_CAT 1 ATRX_CAEEL 1 RS6_AEDAE 1 RSM_CHICK 1 UBF1_KENLA 1 NFM_HUMAN 1 T2FA_HUMAN 1 T2FA_HUMAN 1 TFH_HUMAN 1 NFH_HUMAN | Q24168 07778 P1283 Q9u7ec Q9u766 P16052979 P25979 P07199 P35265 Q35865 P12038 | 1087 | 1020 | 1095 | 517 | 915 | 677 | 857 | 346 | 1359 | 845 | 810 | 618 |
| ORC2_DROME ORC2_DROME ORC2_NROME OVIN NFM_BOVIN NFM_RAT ATRX_CAEEL ATRX_CAEEL ATRX_CAEEL ATRX_CAEEL ANDAC OBP1_XENIA NFM_BUMAN T2FA_HUMAN T2FA_HUMAN NEB1_RAT NFH_HUMAN NEB1_MOUSE | Q24168 07778 P1283 Q9u7ec Q9u766 P16052979 P25979 P07199 P35265 Q35865 P12038 | 1 | _ | ب | 1 | ب | 1 | H | ب | _ | _ | - | ب |
| | Q24168 Q77783 P12839 Q9u7e0 Q9u761 P16053 P25979 P07197 P35269 Q35867 P13036 | NFH_MOUSE | NFH_HUMAN | NEB1_RAT | T2FA_HUMAN | NFM_HUMAN | UBF1_XENLA | NFM_CHICK | RS6_AEDAE | ATRX_CAEEL | NFM_RAT | NFM_BOVIN | ORC2_DROME |

ALIGNMENTS

| O T T T T T X | 488888888888888888888888888888888888888 | FRESOLT FRESULT FRESUL | , |
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| U15038; AAA P20071; IFK P70071; IFK Pro; IPR0011 PF00254; FK TE; P500453; TE; P500453; TE; P500453; TE; P500453 1 | J. BIOI. Chem. 209:30828-30834(1994). -i- FUNCTION: BINDS TO, AND IS INHIBITED BY DOUBLE-STRANDED DNA IN VITRO. PPIASES ACTIVITY: CIS-TRANS ISOMERIZAY PEPTIDE BONDS IN OLIGOPEPTIDES. -i- SUBCELLULAR LOCATION: Nuclear KINASE PTM: PHOSPHORYLATED BY A NUCLEAR KINASE AND ATP. -i- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIAS SWISS-PROT entry is copyright. It is phothern the Swiss Institute of Bioinformat, the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-slb.ch). | LT _SP 01 01 15 46 46 46 15 15 15 15 15 15 15 15 15 15 | |
| Plase. SE_1; FALSE_NE SE_2; 1 SE_3; 1 SE_3; 1 r protein; DNA ASP/GLU-RICH LYS-RICH (BA ASP/GLU-RICH LYS-RICH (BA ASP/GLU-RICH LYS-RICH (BA ASP/GLU-RICH LYS-RICH (BA ASP/GLU-RICH LYS-RICH (BA) PPIASE, FKBP PPIASE, FKBP | TED BY FK506 AND RAPANYC ASES ACCELERATE PROTEIN MERIZATION OF PROLINE IN KINASE IN THE PRESENCE O YPE PPIASE FAMILY. Is produced through a formatics and the EMBL formatics and the EMBL in There are no restriction as its content is smoved usage by and formoved usage by the formoved us | PER 34_SPOFR STANDARD; PRT; 412 AA. 2486; | |

Query Match

17.5%; Score 224; DB 1; Length 412;

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            RESULT 2
FKB4_DROME
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                                                                                                                                                   Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burtlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W. Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Buster M., Gorg F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Buster M., Gu Z., Guan P., Harris M., Glasser K., Buster M., Gu Z., Guan P., Harris M., Glasser K., Buster M., Gu Z., Guan P., Harris M., Gu Z., Guan P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKR4_DROME STANDARD; PRT; 357 AA.
P$4397; Q9VF88;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
39 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans isomerase) (PPiase) (EC 5.2.1.8).
FK506-BP1 OR FKBP39 or CG6226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                   Hostin
                                                                                                                                      Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theopold U., Dal Zotto L., Hultmark D.;
"FKH939, a Drosophila member of a family of proteins that
immunosuppressive drug FK506.";
Gene 156:247-251(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CANTON-S;
MEDLINE-95278752; PubMed-7538962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ephydroidea; Drosophilidae; Drosophila, NCHI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Pterygota; Neoptera;
            Lasko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
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P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lei Y., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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1; Mismatches
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ches 91;
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A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Mount S.M., Moy M., Murphy B., Murphy L., Dr., Pori V., Reese M.G.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J.,
A Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Weilliams S.M., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A Clabs R.A., Myers E.W., Rubin G.M., Venter J.C.,
Branch C., Staple G., Procede C., Procede
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Best Local
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CONFLICT
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-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003708; AAF55172.1; AIT_SEQ HSSP; P27124; 1ROT.
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Pfam; PF00254; FKBP; 1.
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SIMILARITY: BELONGS TO THE FKHP-TYPE PPIASE FAMILY.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE BONDS IN OLIGOPEPTIDES.
SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED, HIGHEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
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  EEEPTPKKPASSKKRANETTPKAPV-----
                                                                                                                                                                      IPQLFCDLVFDK-EFELSHTWGKGSVYFVGYKTPNIEPQGYSEEREEEEEEEEVPAGNAAKA 121
                                                                                                                                                                                                                                     FWGLNMKPERKYSQTIIKS -- FHISGVAL
                                                                                                                                                                                                                                                                              FWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLSTEN 62
                                                                                           VAKPKAKPAEVKPAVDD-----EEDESDSD-----
                                                                                                                                       IPQVALDLNFSKGDRIMFYTAGDASVSLLGYL-----HDIDSEDDEDDDQMTIENLLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z46894; CAA86996.1; -.
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119
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                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKBP_PPIASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
357
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
183
                                                                                                                                                                                                                                                                                                                                                                                                                                                   39343
                                                                                                                                                                                                                                                                                                                                                     15.0%;
25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FK506-bp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥
                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                            Score 191.5; DB 1
Pred. No. 1.4e-05;
2; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASP/GLU-RICH (HIG
ASP/GLU-RICH (HIG
LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                              PPIASE, FKBP-TYPE.
A -> R (IN REF. 1).
EF0AB7831738BB30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FALSE_NEG
                                                                                                                                                                                                                                   -----DKGQEAKLYLAAEKQEYIVATV-TKA
SAKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALL STAGES OF
                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                               110;
                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DURING
  - KVAVTPOKTDEKK
                                                                                       GMDEDDSDGEDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLEABIT
                                                                                                                                                                                                                                                                                                                                                                             357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKBP506
                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
                                                                                                                                                                                                                                                                                                                            Caps
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RESULT 3
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                                                                                                                              Query Match
Best Local
                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1988 (Rel. (01-APR-1988 (Rel. (01-APR-1988 (Rel. (01-1)))))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPM_XENLA
P07222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt-Zachmann M.S., Huegle-Doerr B., Franke W.W.;

*A constitutive nucleolar protein identified as a member of nucleoplasmin family.";

EMBO J. 6:1881-1890(1987).

-I- FUNCTION: ASSOCIATED WITH NUCLEOLAR RIBONUCLEOPROTEIN ST AND BIND SINGLE-STRANDED NUCLEIC ACIDS. IT MAY FUNCTION ASSEMBLY AND/OR TRANSPORT OF RIBOSOME (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                     DOMA I N
                                                                                                                                                                                                                                                                                                                                                Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X05496; CAA29046.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88004394; PubMed=3308448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleophosmin (NPM) (Nucleolar phosphoprotein
                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                             Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kenopodinae; Kenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004301; Nucleoplasmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleolar protein NO38).
  166
                            143
                                                         107
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                                                                                    E 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        A29681; A29681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGGKAANQSPKSASQVSCGSCKKTFNSGNALESHNKAKHAAAK 245
                                                      GSGPYYVSGQHLVALEDLESSDDEDEEHEPSPK-NAKRIAPDSASKVPRKKTRLEEEEED 165
                                                                                 GKGSVYFVGYKTPNIEPOGYSEEEEEEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEEDE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAKKEQPKAKEPAKQQPASKDPRTITGGVKIVDQVVGKGEEAK 267
SDEDDDDDDDDDDDDDEEEEETPVKKTDSTKSKAAQKLNHNGKASALSTTQKTPKTPEQ
                            SD-SDGMDEDDSDGEDSEEEEPTP-KKPASSKKRA-----NETTPKAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EESGEEDEQDSDDSEAEEEQPKAKVAKLSPGASAKKSGKEQNGVAKKEEAKQQQKKKEKP 224
                                                                                                                                                                                                                                                                                                                                                            PF03066; Nucleoplasmin;
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                Conservative
                                                                                                                                                                                                                                           160
189
218
218
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                                                                                                                                                                                                                                                                                                                                            Phosphorylation; RNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07, Created)
07, Last sequence update)
39, Last annotation updat
                                                                                                                                                                                                   137
158
187
195
242
220
223
239
                                                                                                                                                                                      33532 MW;
                                                                                                                           13,3%;
31.5%;
                                                                                                                20;
                                                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ASP/GLU-RICH (HIGHLY ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
4 X 3 AA REPEATS OF K-T-P.
                                                                                                                           Score 170.5; DB 1
Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                    C16CDF9565090843 CRC64;
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pipoidea; Pipidae;
                                                                                                                                         DB 1;
                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B23) (Numatrin)
                                                                                                                                        Length
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURES
                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
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                                                                                                            Gaps
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RESULT 4
NUCL_CHICK
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                DOMAIN
DOMAIN
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MEDLINE-89119560; PubMed-2914325;
BOFER R.A., Lehner C.F., Eppenberger H.M., Nigg E.
"Major nucleolar proteins shuttle between nucleus
Cell 56:379-390(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                         Pfam; PF00076; rrm; 4. SMART; SM00360; RRM; 4.
                                                                                                                                                                                               EMBL; X17199; CAA35060.1; -. EMBL; M21791; AAA48983.1; -. FIR; S08414; DNCHNL.
                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maridor G., Krek W., Nigg E.A.;
"Structure and developmental expression of chicken nucleolin NO38: coordinate expression of two abundant non-ribosomal nucleolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleolin (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCL_CHICK P15771;
                                                                                  Nuclear protein; RNA-binding
                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1049:126-133(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISCUSSION OF SEQUENCE.
MEDLINE-90304215; Pubme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 18:1286-1286(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maridor G., Nigg E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90206792; PubMed-2320420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
  DOMAIN
                                                                                                                                                                                     HSSP; P09651; 1UP1.
                                                                                                                 PROSITE; PS00030;
                                                                                                                             PROSITE;
                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA sequences of chicken nucleolin/C23 and NO38/B23, two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 KGKQDTKPQTPKTPKTPLSSEEIKAKMQTYLEKGNVLPKVEVKFANYVK -- NCFRTEN
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR CHROMATIN AND PREFIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLAY
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                     ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME ASSEMBLY. SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKK - - - - - -
                                                                                                                             PS50102;
                                                                                                                                                                      IPR000504; RRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins.
 124
170
217
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281
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461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                               Phosphorylation; Methylation; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed-2114180;
                                                                                                                 RRM_RNP_1;
                                                                                                                             RRM; 4
  141
192
247
357
445
535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
ASP/GLU-RICH
ASP/GLU-RICH
ASP/GLU-RICH
RNA-BINDING (
RNA-BINDING (
                                                                                                                 w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abundant non-ribosomal nucleolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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 (RRM)
                                       H (ACIDIC).
H (ACIDIC).
H (ACIDIC).
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                                                                                                                                                                                                                                                                                                                                                                                                                  TO PLAY
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P16039;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
MOD_RES
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REPEAT
REPEAT
                                                                                             BIOCHIM. BIOPHYS. ACLA 1049:126-133(1990).

-I- FUNCTION: ASSOCIATED WITH NUCLEOLAR RIBONUCLEOPROTEIN STRUCTURES AND BIND SINGLE-STRANDED NUCLEIC ACIDS. IT MAY FUNCTION IN THE ASSEMBLY AND/OR TRANSPORT OF RIBOSOME.

-I- SUBCELLULAR LOCATION: NUCLEAR. GENERALLY NUCLEOLAR, BUT IS TRANSLOCATED TO THE NUCLEOPLASM IN CASE OF SERUM STARVATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                         proteins.
                                                                                                                                                                                                                                               NO38:
                                                                                                                                                                                                                                                                                                     MEDLINE-90304215;
                                                                                                                                                                                                                                                                                                                      DISCUSSION OF SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    nucleolar proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90206792; PubMed-2320420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPM_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                            Maridor G., Krek W., Nigg E.A.; "Structure and developmental expression of chicken nucleolin
                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 18:1286-1286(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                           Marldor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_Tax ID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria;
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01-AUG-1988 (Rel. 08, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                       "A major nucleolar protein, nucleolin, induces chromatin decondensation by binding to histone H1."; Eur. J. Biochem. 175:525-530(1988).
-i- FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLADECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLADECONDENSATION BY BINDING TO HISTONE H1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 35-713 FROM N.A., AND MEDLINE-87175501; PubMed-3470736; Lapeyre B., Bourbon H., Amalric F.
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                    Erard M.S.,
Amalric F.;
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ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS. SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIF
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ASP/GLU-RICH (HIGHLY ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
B1FF89B5F2322DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;
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PROSITE; PS00030; RRM_RNP_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 213-294 FROM N.A., AND SEQUENCE OF 227-294.
MEDLINE-87033628; PUDMed=2429957;
Chan P.-K., Chan M.-Y., Yung B.Y.M., Cook R.G., Aldrich M.B.,
Ku D., Goldknopf I.L., Busch H.;
"Amino acid sequence of a specific antigenic peptide of prote
J., Biol. Chem. 261:14335-14341(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFDLINE-89374300; PubMed-2775293;
Li x., McNeilage L.J., whittingham S.;
"The nucleotide sequence of a human cDNA encoding conserved nucleolar phosphoprotein B23.";
Blochem. Biophys. Res. Commun. 163:72-78(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene: identification of the
region.";
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Chan P.-K., Chan F.Y., Morris S.W., Xie Z.;
*Isolation and characterization of the human
gene: identification of the YYI binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA from interferon-treated cells encoding nucleolar protein
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MEDLINE-90026373; PubMed-2478125;
Zhang X.T., Thomis D.C., Samuel C.E.;
"Isolation and characterization of a !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of the cDNA encoding human nucleophosmin and studies of its role in normal and abnormal growth.";
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Chan P.-K.;
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MEDLINE=89229105; Pubi
Chan W.-Y., Liu Q.R.,
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                                              SEQUENCE OF 1-117 FROM N.A.
MEDLINE-96210614; PubMed-8633037;
Fujimoto J., Shiota M., Iwahara T.,
                                                                                                                                                              Morris S.W., Kirstein M.N., Valentine Shapiro D.N., Saltman D.L., Look A.T., Fusion of a kinase gene, ALK, to a nu non-Hodgkin's lymphoma.", Science 263:1281-1284(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numan protein B23.";
Nucleic Acids Res. 17:10112-10112(1989).
[6]
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                                                                                                                                                                                                                                                                                               rissUE-Lymphoma;
MEDLINE-94167588; PubMed-8122112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a cDNA clone representing a third allele numan protein B23.";
Characterization of the transforming activity of p80,
                                                                                                                                                                                                                                                                                                                                                                 EQUENCE
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.R., Borjigin J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commun. 164:176-184(1989).
                                                                                                                                                                                                                    a nucleolar protein gene,
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                                                      Seki N.,
                                                                                                                                                                                                                                                                           M.B., Dittmer K.G.,
                                                      Satoh H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide of protein B23.";
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J1 H., Reid G.E., Moritz R.L., Ed
J1 Ko-dimensional gel database
"A two-dimensional gel database
Electrophoresis 18:605-613(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodner R.L., Rush E.A., Faas S., Rudert W.A., Corey S.J.; "The t(5;17) variant of acute promyelocytic leukemia expresses nucleophosmin retinoic acid receptor fusion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperphosphorylated protein in a Ki-1 lymphoma cell line with chromosomal translocation t(2;5).";
Proc. Natl. Acad. Sci. U.S.A. 93:4181-4186(1996).
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DISEASE: PARTICIPATES IN A T(3;5)(Q25.1;Q34) CHROMOSOMAL

TRANSLOCATION. THE PRODUCT, A NPM-MLF1 FUSION PROTEIN, IS

RESPONSIBLE FOR MYELODYSPLASTIC SYNDROME (MDS) WHICH PROGRESSES

ACUTE MYELOID LEUKEMIA (AMI.).
                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREATMENT WITH ANTICANCER DRUGS.
PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                      non-profit institutions as long
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                                                                                                                                                         AAA36380.1;
AAA58386.1;
AAA36385.1;
 AAB94739.
AAB34739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORM OF NON-HODGKIN'S LYMPHOMA TRANSLOCATION T(2;5)(P23;Q35)
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EMBL; U44946; AAA5865
EMBL; D45915; BAA0884
EMBL; U41742; AAB0011
EMBL; U41743; AAB0011
PIR; A30137; A3137
PIR; A32915; A33915
PIR; A26080; B26080
PIR; B26080; B26080
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PIR; A33423; A33423
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30-MAY-2000 (Rel. 39, Last sequence up
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Mitotic apparatus protein P62.
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                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-97166213; PubMed-9013612;
                                                                                                                                                                                                      NCBI_TaxID-7653;
                                                                                                                                                                                                                             Lytechinus
                                                                                                                                                                                                                                                 Echinoidea;
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J004946; AAA58698.1;

D45915; BAA08343.1;

J041742; AAB00112.1;

J041743; AAB00113.1;
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                                                                                                                                                                                                                                                 Euechinoidea;
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E -> D (IN REF. 10).

D -> P (IN REF. 6).

P -> S (IN REF. 6).

P -> S (IN REF. 6).

TPR -> SSS (IN REF. 6).

W; 620BC7BA2E4A0054 CRC64;
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"Molecular characterization of p62, a mitotic apprequired for mitotic progression.";
J. Biol. Chem. 272:3506-3614(197).
-I- FUNCTION: REQUIRED FOR MITOTIC PROGRESSION.

apparatus

protein

BINDS

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CHROMATIN

SUBCELLULAR PTM: PHOSPHO

PHOSPHORYLATED

LOCATION: Nuclear

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CAM-KINASE

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Ye X., Sloboda R.D.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
               MEDLINE-89121496;
                                                                               Bourbon H., Lapeyre B., Amairic F. Structure of the mouse nucleolin
                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nucleolin (Protein C23).
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                              SEQUENCE OF 1-44 FROM N.A.
                                                                                                          MEDLINE-88316930; PubMed-3137346;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                      Mus musculus (Mouse).
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                                          each RNA binding domain is encoded ol. Biol. 200:627-638(1988).
                                                                                                                                                                                                                                                                                                                                                                  KRKVPNGSVENGHAIDDDEDDEEDEDYKVGDE 262
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  Prudhomme M.,
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POLY-G
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POLY-A
                PubMed-2906027
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Rodentia;
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  Amalric F.;
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POLY-GLU.
POLY-ASP.
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                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR000504; RRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cleaves nucleolin in vitro. "
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MEDLINE=91317840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and structure of the nucleolin promoter in rodents: characterization of a strikingly conserved CpG island."; Gene 68:73-84(1988).
                                                                                                                                                                                                                                                                                                                                                               Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A29958;
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PROSITE; PS00030; RRM_RNP_1; 3.
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FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWI EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLA CHOMATIN AND PREBIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PROLE IN PRE-FRNA TRANSCRIPTION AND TRIBOSOME ASSEMBLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
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NKKG-----EFVPLHVKVGNQNLVLGTLSTENIPQLFCDLVFDKEFELSHTWGKGSVYFV
                                         IEVKSGKPVTVTPEEGILI---
                    IPQKKGKKATTTPAKKVVVSQTKKAAVPTPAKKAAVTPGKKAVATPAKKNITPAKVIPTP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                     P09651;
                                                             61;
                                                                       Similarity
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24.1%;
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RNA-BINDING
RNA-BINDING
RNA-BINDING
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Pred. No. 0.007
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ASP/GLU-RICH
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[l proteins. Granzyme
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SMART; SM00360; RRM; 4.
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-i- FUNCTION: NUCLEGULN IS THE MAJOR NUCLEGUAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEGUAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90368666; PubMed-2394707; Srivastava M., McBride O.W., Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Srivastava M., Fleming P.J., Po
"Cloning and sequencing of the
FEBS Lett. 250:99-105(1989).
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01-MAR-2002
                                                                  RNA-binding.
                                                                                        Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
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ASP/GLU-RICH
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"Sequence and structure of the nucleolin pucharacterization of a strikingly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90269607; PubMed-2347493;
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                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-44 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Gene
                                                                                                                                                                                                                                                                                                                                                                                 "Nucleolin gene organization in rodents: highly conserved sequences
within three of the 13 introns.";
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                                                                          ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME ASSEMBLY SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS. SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                      e 68:73-84(1988).
FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLA
                  SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                              88:187-196(1990)
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RNA-BINDING (RRM)
RNA-BINDING (RRM)
RNA-BINDING (RRM)
ARG/GLY/PHE-RICH.
B x 8 AA TANDEM RX-X.
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Pred. No. 0.00
9; Mismatches
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EMBL; M55015; AAA41732.1; JOINED.
EMBL; M55017; AAA41732.1; JOINED.
EMBL; M55020; AAA41732.1; JOINED.
EMBL; M250209; AAA41733.1; -.
EMBL; M22090; AAA41733.1; -.
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                                                                                                                                                                                                                                               and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARG/GLY/PHE-RICH.
8 x 8 AA TANDEM REPEATS OF X-T-P-X-K-K-X-X-X.
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"Cloning of a cDNA encoding a novel
          NCBI_TaxID=9986;
                                                                                  NEF3 OR NEFM OR NFM.
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"Cloning of a control of the control
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p1-0CT-1996 (Rel. 34, Last sequence update)
p16-0CT-2001 (Rel. 40, Last annotation update)
p16-0CT-2001 (Rel. 40, Last annotation update)
p16-0CT-1001 (Rel. 40, Last annotation update)
p17-0CT-1001 (Rel. 40, Last annotation update)
p18-0CT-1001 (Rel. 34, Created)
p19-0CT-1996 (R
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mold).
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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolao
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P13084; Q64269; Q63998;
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
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Viladello M., Vetlore S., Lamar E., Chien K.R., Gorza L.;

"Neurofilament M mRNA is expressed in conduction system myocytes of the developing and adult rabbit heart.";

J. Mol. Cell. Cardiol. 28:1833-1844(1996).

-i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

-i- PTM. THERE ARE A NUMBER OF THE MAINTENANCE IN THIS MOTIF. IT IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
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PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTOF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                         Similarity
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                          B23) (Numatrin)
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8 CRC64;
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                                                                                                                                                                                                                                                                                                                                          Indels
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"Structure of the gene for rat nucleolar protein B23.";

J. Biol. Chem. 265:18227-18233(1990).

-i- FUNCTION: ASSOCIATED WITH NUCLEOLAR RIBONUCLEOPROTEIN STRUCTURES AND BIND SINGLE-STRANDED NUCLEIC ACIDS. IT MAY FUNCTION IN THE ASSEMBLY AND/OR TRANSPORT OF RIBOSOME.

-i- SUBURIT: DISULFIDE-LINKED DIMERS UNDER CERTAIN CONDITIONS.
-i- SUBURIT: DISULFIDE-LINKED DIMERS UNDER CERTAIN CONDITIONS.
-i- SUBCELLULAR LOCATION: NUCLEAR. GENERALLY NUCLEOLAR, BUT IS
                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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MEDLINE-88330763; PubMed-3417636;
Chang J.-H., Dumbar T.S., Olson N
                                                                                                                                                                                                EMBL; J04944; AAA40793.1; PIR; A28939; A28939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-91009311; PubMed-2211699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cDNA and deduced primary structure of rat pr
protein containing highly conserved sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus ()
Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                                                                                                                                 Pfam; PF03066; Nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89308567; PubMed-2745414; Chang J.-H., Olson M.O.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (B23.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A single gene codes for two forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSLOCATED TO THE NUCLEOPLASM IN CASE TREATMENT WITH ANTICANCER DRUGS. ALTERNATIVE PRODUCTS: 2 ISOFORMS; B23.1
                                                                                                                                                                                                                               ; M37038; AAA41731.1;
; M37040; AAA41731.1;
; M25062; AAA40795.1;
; J04943; AAA40794.1;
                                                                                                                                                                                                                                                                                                                                                                   M37039;
M37035;
M37036;
M37037;
M37038;
                                                                                                                                                                                                                                                                                                   M37036;
M37037;
                                                                                                                                                                                                                                                                                                                                      M37041;
M37035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J03969;
                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Swiss Institute of Bioinformatics
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                                                                                                                                                                                  IPR004301;
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AAA41730.1;
AAA41730.1;
AAA41730.1;
AAA41730.1;
AAA41731.1;
AAA41731.1;
AAA41731.1;
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AAA41731.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263:12824-12827(1988)
                                                                                                                                                 Phosphorylation;
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                                                                                                                                                                 leoplasm:
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     license agreement (See http://www.isb-sib.ch/announce/
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        MET-RICH.

ASP/GLU-RICH (ACIDIC).

NUCLEAR LOCALIZATION SIGNAL (HIGHLY ACIDIC).

ASP/GLU-RICH (HIGHLY ACIDIC).

NUCLEAR LOCALIZATION SIGNAL (RICHEAR LOCALIZATION SIGNAL (RICHEAR HOSPHORYLATION).

PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOFORMS; B23.1 (SHOWN HERE) AND B23.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.O.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                              RNA-binding; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleolar protein
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                             (BY CK2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the
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                                                              (POTENTIAL)
                                                                                                                                                splicing
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nucleolar phosphoprotein pl30 (Nucleolar 130 kDa protein) (140 nucleolar phosphoprotein) (Nopp140) (Nucleolar and coiled-body phosphoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP14_RAT
P41777;
           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                 Yang Y., Isaac C., Wang C., Dragon F., Pogacic V., Meler U.T.; "Conserved composition of mammalian box H/ACA and box C/D small nucleolar ribonucleoprotein particles and their interaction with common factor Nopp140.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92323542; PubMed=1623516; Meier U.T., Blobel G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH NOP5 AND FIBRILLARIN. MEDLINE-20143579; PubMed-10679015;
                                                                                                                                                                                                                                                                                                                                                                                                     "Nopp140 shuttles on tracks between nucleolus Cell 70:127-138(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
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                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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39; Conserv
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; 1372A474F9ED2457 CRC64;
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                                                                               gh a collaboration - EMBL outstation -
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                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                              103 SEEEEEEEEEPPAGNAAKAVAKPKAKPAEVKPAVDDEEDESDSDGMDEDDSDGEDSEEEE 162
KAAAESSSSSSSEDSSEEEKKKPKSKA 543
                   QVSCGSCKKTFNSGNALESHNKAKHAAA 244
                                        ARVTAKAAPSLPAKQAPRAGGDSSSDSESSSSEEEKKTPPKPPAKKKAAGAAVPKPTPVK
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                                                                                                                                                                   Conservative
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MISSING (IN NOPP140B).
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C SERINE CLUSTER 1.
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C SERINE CLUSTER 10.
C SERINE CLUSTER 11.
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Search completed: May 2, 2002, 22:31:08 Job time: 1414 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Sequence:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1279
1274
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1: sp_archea:*
2: sp_bacteria.
3: sp_fungt:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
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9: sp_phage:*
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11: sp_rodent:
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| Q950V3 nomo sapien Q06459 xenopus lae | TO COURTS | 7 | | | ١ |
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| nomo | 13 006450 | 705 | 10.8 | 138 | , |
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| Q96j17 homo sapien | 4 Q96J17 | 418 | 10.8 | 138 | ω. |
| Q9xvs4 caenorhabdi | 5 Q9XVS4 | 971 | 10.8 | 138.5 | ~ |
| Q9vnx6 drosophila | 5 Q9VNX6 | 688 | 10.8 | 138.5 | |
| Q917q2 streptococc | 16 Q9L7Q2 | 1881 | 11.0 | 140.5 | _ |
| Q90307 carassius a | 13 Q90307 | 798 | 11.0 | 140.5 | • |
| Q9su25 arabidopsis | 10 098025 | 649 | 11.0 | 140.5 | w |
| 09c2f7 neurospora | 3 Q9C2F7 | 305 | 11.1 | 142.5 | 7 |
| Q00880 haematonect | 3 Q00880 | 507 | 11.3 | 144 | ٠. |
| Q9dav3 mus musculu | | 285 | 11.3 | 144 | ٠. |
| Q9day9 mus musculu | 11 Q9DAY9 | 257 | 11.3 | 144 | _ |
| Q26711 trypanosoma | 5 Q26711 | 312 | 11.4 | 145.5 | ~ |
| 045181 caenorhabdi | 5 045181 | 798 | 11.5 | 146.5 | .~ |
| Q91802 xenopus lae | 13 Q91802 | 296 | 11.6 | 148 | _ |
| Q9y2d9 homo sapien | 0 | 606 | 11.7 | 150 | _ |
| | 11 Q9QZX1 | 715 | 11.8 | 151.5 | • |
| | 10 040363 | 635 | 12.0 | 153.5 | |
| | 4 Q96DC4 | 265 | 12.0 | 153.5 | ~ |
| homo | 4 Q96EA5 | 294 | 12.1 | 155 | ٠. |
| homo | 4 Q9BYG9 | 259 | 12.1 | 155 | • |
| Q9bti9 homo sapien | 4 Q9BTI9 | 214 | 12.1 | 155 | _ |
| homo | 4 Q9NX34 | 179 | 12.1 | 155 | _ |
| | | 444 | 12.2 | 155.5 | ٠٠ |
| Q91255 petromyzon | 13 Q91255 | 1110 | 12.3 | 157 | |
| Q9nlm3 asterina pe | 5 Q9NLA3 | 346 | 12.3 | 157 | _ |
| | 4 Q96AT6 | 294 | 12.3 | 157 | _ |
| chire | 5 Q95PU8 | 513 | 12.4 | 158.5 | _ |
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| | 028; ZINC_FINGER_C2H2_1; 1. | PROSITE; PSO | 뮸 |
| | SMART; SM00355; ZnF_C2H2; 1. | SMART; SM0035 | DR |
| | InterPro; IPR000822; Znf-C2H2. | InterPro; IP | DR |
| | 2.1; | EMBL; AF19554 | DR |
| | I-1999) to the EMBL/GenBank/DDBJ databases. | Submitted (OCT-1999) to | ŖĽ |
| | • | Arabidopsis thaliana."; | RT. |
| ם | | "Functional a | RT. |
| | Wu K., Tian L., Malik K., Brown D., Miki B.; | Wu K., Tian I | ₽ |
| | LUMBIA; | STRAIN-CV. COLUMBIA; | RC |
| | N.A. | SEQUENCE FROM N.A. | RP |
| | | [1] | R |
| | | NCBI_TaxID=3702; | o X |
| e, noerdac, | Brassicales; Brassicaceae; Arabidopsis. | eurosids II; Brassicales; | 88 |
| e. Poeidao. | Spormatophyta: Margollophyta: Budicoty Bedons: ora Budicots: Bosidapo | Spermatonhyta | 3 8 |
| pophyta. | Enkarvota: Viridinlantae: Strentonbyta: Embryonbyta: Trache | Enkarvota: Vi | 38 |
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Pfam; PF00096; zf-C2H2; 1.

SMART; SM00355; znf-C2H2; 1.

PR0SITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS050157; ZINC_FINGER_C2H2_1; 1.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.

SEQUENCE 257 AA; 27698 MW; C440438761
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de la Bastide M.R., Parnell L.D., Kaplan N., Gnoj L., Hameed A.,
Schutz K., Hasegawa A., Gottesman T., Shohdy N., Granat S., Jenss
Johnson A.F., Lodhi M., Dedhia N., Martienssen R., McCombie W.R.
A. thaliana BAC T32N15 from chromosome V.*;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC002534, AAB70032.1;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core e
eurosids II; Brassicales; Brassicacea; Arabidopsis.
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Best Local S
Matches 151
                             049209 PRELIN
049209;
01-JUN-1998 (Trem
01-JUN-1998 (Trem
01-DEC-2001 (Trem
PUTATIVE HISTONE I
HD2 OR HD2B
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Q1-MAR-2001 (TrEMBLrel. 16, Last sequence up
Q1-MAR-2001 (TrEMBLrel. 19, Last annotation
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
HISTONE DEACETYLASE-LIKE PROTEIN.
AT5G22650 OR MDJ22.7.
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STRAIN-COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
MAKAMURA Y., Sato S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, A8065699; BAB11671.1;

EMBL, A8065993; AAL24375.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,044,062
physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnollophyta; eudloctyledons;
eurosids II; Brassicales; Brassicaceae; Arabic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                             EKKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSN
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8 (TrEMBLrel. 06, La
1 (TrEMBLrel. 19, La
ISTONE DEACETYLASE.
       thaliana
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50.5%;
   (Mouse-ear cress)
                                                                                                06, Created)
06, Last sequence up
19, Last annotation
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Pred. No. 1.1e
24; Mismatches
                                                                                                                                                                                                                                                  PRT;
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RESULT
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Best Local S
Matches 151
                                                                                             plants.";
Submitted
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Q9M4U5;
01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
HISTONE DEACETYLASE 2 ISOFORM B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AFO
EMBL; AFO
SEQUENCE
EMBL; AF254072; AAF68624.1; ...
InterPro; IPR000822; Znf-C2H2.
SMART; SM00355; ZnF_C2H2; 1.
PROSITE; PS0002B; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 303 AA; 32613 MW; 708E46271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu K., Tian L., Malik K., Brown D., Functional analysis of HD2 histone arabidopsis thaliana.", Submitted (OCT-1999) to the EMBL/Ger EMBL; AF044914; AAC02539.1; -... EMBL; AF195546; AAG28473.1; -...
                                                                                                                                      SEQUENCE FROM N.A. Dangl M., Brosch G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dangl M., Haas H., Loidl P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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[1]
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                                                                                                                                                                                                                        Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                              Panicoideae;
                                                                                                                                                                                                         Spermatophyta; Magnoliophyta;
                                                                                                                           "Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                   UT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPT
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                                                                                               (APR-2000)
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                                                                                                                                                                                            Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKGGKA---ANQSPKSASQVSCG-SCKKTFNSGNAL-ESHNKAKH
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50.78;
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                                                                                                                           Haas H., Loidl
ization of type
                                                                                                                                                                                              Zea.
                                                                                               EMBL/GenBank/DDBJ
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                                                                                                                                                                                                           Liliopsida;
                                                                                                                        Loidl P., Lusser type-2 histone
  708E4627101BB67C CRC64;
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deacetylase homologs
                                                                                                                                      Lusser
                                                                                                                                                                                                         Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC cl
                                                                                                                                                                                                                                                                update)
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                                                                                               databases
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Q9M4T4;
Q9M4T4;
Q1-QTT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 19, Last annotation update)
PUTATIVE HISTONE DEACETYLASE HD2C (AT5G03740/F17C15_160).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
       Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR255712; AAR70197.1; -
                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
STRAIN-COLUMBIA;
MEDLINE-97471969; PubMed-9330910;
MEDLINE-97471969; Nakamura Y.,
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Dangl M., Brosch G.,
                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      "Structural
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Molecular characterization
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AB005235;
AF372889;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ da
EMBL; AF255711; AAF70196.1; -.
InterPro; IPR000822; Znf-C2H2.
SMART; SM00355; ZnF_C2H2; 1.
PR0SITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Metal-binding; Zinc-finger,
SEQUENCE 297 AA; 32502 MW; EEB3AAC0D2C41C63
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Q9M4T5;
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SMART; SM
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Ehrhartoideae; Oryzeae; Oryza.
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Eukaryota: Viridiplantae:
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE HISTONE DEACETYLASE HD2.
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PROSITE; PS50157; ZINC_FINGER_C2H2_1; 1.
DNA-binding; Metal-binding; Zinc-finger,
SEQUENCE 294 AA; 31830 MW; 7B69F3BE8
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                                                                                                                                                                                                                                                                                           "Molecular
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DKFPQIQFDLVFDKEFELSHTSKTASVFFSGYKVSQPAEEDEMDFDSEEVEDEEEEEKII
                         ENIPOLICOLYEDKEFELSHTWCKCSYYFYCYKT -- PNIEPQ ----- GYSEEEEEEEEE
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                                                                                                        Conservative
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yta; Liliopsida; Poales; Po
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Pred. No. 3.6e
33; Mismatches
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                                                                                                                   511.5; DB 1
No. 5.1e-31;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HISTONE DEACETYLASE-LIKE PROTEIN.
F17C15_160. thiltena /Mouse-ear cress).
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submitted (MAR-2000) to the EME
EMBL; AL162506; CAB82939.1; -
Interpro; IPRO00822; Znf-C2H2.
SMART; SM00355; ZnF_C2H2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LZR5
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 296 AA: 32129 MW; 4B2DAABE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  WGLLYPPAAPKSAAKQVNFQLPNEDVKAKQDDDADGSEEDSSDDDDSENSGDEEEEKVTA 170
                                                                                                                                                                                                                                                                                                                                                                                                                              ENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEEVPAGNAAK 120
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                                                   AKHAAA
                                                                                               KPHVHVATPHPSKQAGKNSGGGSTGETSKQQQTPKSAGAFGCKSCTRTFTSEMGLQSHTK
                                                                                                                                                                                                  ESDSEEDDSSDDEEDDSSEEETPKKPEEPKKRSAEPNSSKNPASNKKAKF-VTPQKTDSK
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, Mayer K.F.X.;
  295
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                                                                                                                                                                                                                              -DGEDSEEEEPTPKKPASSKKRANE-TTPKAPVSAKKAKVAVTPQKTDEK
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39.5%;
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he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 498.5;
Pred. No. 4.9e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                 -EVKPAVDDEEDESDSDGMDEDDS---
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                                                                                                                                              NOSPKSASOVSCGSCKKTFNSGNALESHNK 238
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nes 81;
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Best Local S
Matches 128
                                                                                                                                                                                                 024591;
024591;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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Eukaryota: Viridiplantae: Streptophyta:
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01-CCT-2000 (TremBLrel. 15, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation updat
HISTONE DEACETYLASE 2 ISOFORM C.
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                                                                 Zea mays (Maize).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Panicoldeae; Andropogoneae; 20
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SMART; SM00355; ZnF_C2H2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     024591
                                          NCBI_TaxID-4577;
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Molecular characterization of type-2 histone o
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128; Conserv
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                                                                                                                Streptophyta; E
yta; Liliopsida;
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                                                                                 Zea
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Pred. No. 1.3e-29;
5; Mismatches 71
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a; Poales; Poaceae; PACC cl
                                                                                                                a; Poales; Poaceae; PACC cl
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deacetylases
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Best Local
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Q94F81;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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STRAIN-CUZCO 251;
MEDLINE-97349336; PubMed-9204905;
MEDLINE-97349336; PubMed-9204905;
Iusser A., Brosch G., Loidl A., Haas H., Loidl P.
"Identification of maize histone deacetylase HD2 nucleolar phosphoprotein.";
Science 277:88-91(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1997) to the EMBL/GenBa
EMBL; 082815; AAB63362.1; -
EMBL; AF026917; AAC61674.1; -
Interpro; IPR000822; Znf-C2H2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2;
DNA-binding; Zinc_FINGER_C2H2_2;
SEQUENCE 307 AA; 33238 MW; 9CFF6B(
                                             SEQUENCE FROM N.A.
STRAIN=CV B73;
Chandler V.L., Kaeppler S.M., Kaeppler H.F., Cone
"Sequences from the Plant Chromatin Consortium (NS
project 9975930).";
                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                             HD2
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 STRAIN-CV. B73;
            SEQUENCE FROM N.A.
                                    Submitted
                                                                                                                                                                     Zea mays (Maize)
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                                                                                                                     NCBI_{TaxID}-4577;
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                                   (JUN-2001)
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                                                                                                                                                                                                                              (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                               Andropogoneae;
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39.0%;
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EMBL/GenBank/DDBJ
                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                 Created)
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Pred. No. 8.8e-29;
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Best Local :
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Best Local
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE HISTONE DEACETYLASE HD2D.
                                                                                                                                                                                                                                           Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF255713; AAF70198.1; -. SEQUENCE 203 AA; 22651 MW; 69AlDA5941D7A293 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsia.
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01-OCT-2000
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF384033; AAK67143.1;
                                                                                                                                                                                                                                                                                  plants.
                                                                                                                                                                                                                                                                                           Dangl M., Brosch G., Haas H., Loldl P., Graessle S., Lusses Molecular characterization of type-2 histone deacetylases
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
               174
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 RANETTPKAPVSAKKAKVÄVTPQKTDEKKKGGKAANQS-PKSASQVSCG-SCKK 225
                                                                                                                                                         MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGEC-KNKKGEFVPLHVKVGN--QNLVLGT
                                                   AAKAVAKPKAKPAEVKPAVDDEEDESDSD--GMDEDD--SDGEDSEEEEPTPKKPASSKK
                                                                                                           LSTENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEEPPAGN
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                                    EQQIAALPQ---NEINP---EEDDESDSDEMGLDEDDDSSDEEDVEAEAPLKVAPPSKK-
                                                                                    LS-QKFPQFSIDLYLGHEFEISHN-STSSVYLIGYRT--FDAFDELDEEIDSDSELDEYM
                                                                                                                                     MEFWGIEIKPGKPFKVIQKDGFMVHASQVTLGDVEKVKKDETFAVYVKIGDDENGFMIGN
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30808 MW; E295E5CDFE4DEF1A CRC64;
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35.7%;
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8; Mismatches
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Pred. No. 5.
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edons; core eudicots; Rosid
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.9e-16;
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Matches
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Best Local
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                            01-NOV-1996 (Tremblrel 01, 01-NOV-1996 (Tremblrel 01, 01-DEC-2001 (Tremblrel 19, NUCLEOLAR PHOSPHOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY057543; AAL09783.1; -. SEQUENCE 477 AA; 52223 MW; 10C405953B17675E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                           XNOPP180.
                                                                                                                                                                                            Q91803;
                                                                                                                                                                                                                    Q91803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AT4G25340/T30C3_20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAKAVAKPKAKPAEVKPAVDDEEDESDSDGMD----EDDSDGEDSEEEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGFWGLEVKPGKPQAYNPKNEQG-KIHVTQATLGTGLSKEKSVI--QCSIGDKAPIALCS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEFWGIEVKSGKPVTVTP--EEGILIHVSQASLGECKNKKGEFVPLHVKVGNQ-NLVLGT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TPQKTDEKKKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSTENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEEEEEEEVPAGN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                       266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%;
27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GKAANQSPKSASQV-----SCGSCK----KTFNSGNALESHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DYEHDEDDSDGIDVGESEEDDSCEYDSEEDEQLDEFEDFLD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Mismatches
                                                                                                                     Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
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Pred. No. 8.8e-06;
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                                                                                                                                           sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PVEFTVTGDRSIHLSGFLEYYQDDED-----
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Vertebrata;
ia; Pipoidea;
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  Euteleostomi;
; Pipidae;
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RESULT

Q9STK2

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Best Local S
Matches 55
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"Identification and cDNA cloning of a phosphoprotein, xnopp180, that is the protein Nopp140.";
J. Cell Sci. 108:3339-3347(1995).
EMBL; X88927; CAA661368.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 53,3 KDA PROTEIN.
T30C3.20 OR AT4G25340.
T30C3.20 OR AT4G25340.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9STK2;
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NCBI_TaxID=8355;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-96019267;
                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G
EMBL; AL079350; CAB45512.1; -.
EMBL; AL101563; CAB81345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Rose M., Hempel S., Entian K.-D., Be
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                    PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
                                                                                                        InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Rose M., Hempel S., E Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                Hypothetical
                                                                                                                                                              HSSP; Q00688; 1PBK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVTPQKTDEKKKG-----GKAANQSPKSASQVSCGSCKKTFNSGNALESHNKAKHAAAK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDVKQGAKAAKPTPKKAASSSSEDSSSDEDVSKAKKTNTAVSKSPVTTPKAVPAAKKESS 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSEEEGKSKOPTGKSPAAKATAPPKKNPVAVNKDKPSSSSSSSSSGDDEKOKPKOAAAA 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEEEEEEEEVPAGN--AAKAVAKPKAKPAEVKPAVDDEEDESDSDGMDEDDSD----- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GEDSEEEEPTPKKPASSK------
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cal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   opsis sequencing project;
(JUN-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                              Entian K.-D., Mewes H.W., to the EMBL/GenBank/DDBJ
     53290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.98;
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                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165.5; DB 13; Pred. No. 0.0002; 7; Mismatches 64;
     5B2FA21570BC0AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487
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                                                                                                                                                                                                                                                                                                                                              Lemcke K., databases.
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                                                                                                                                                                                                                                                                                                                                                                      Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mewes H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosidae;
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 264
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                                                                                                                                                                                                                                                                                 1 MEFW-------GIEVKSGKPVTVTP--EEGILIHVSQASLGECKNKKGEFVPLHVKV 48
                                                                                                                                                                                                                                                                  MGFWGSDFVLLTYAGLEVKPGKPQAYNPKNEQG-KIHVTQATLGTGLSKEKSVI--QCSI
EQDDGQESANKSK 276
                                                                                                       QLDEFEDFLDSNLERYRNAAAPKSGVIIEEIEDEEKPAKDNK:
                                                                                                                                                                                     EEEEEVPAGNAAKAVAKPKAKPAEVKPAVDDEEDESDSDGMD-----EDDSDGEDSEEEE 162
                                                                                                                                                                                                                 GDKAPIALCSLLPNKIECCPLNLEFDDDDE---
                                                  KQIVAIEGAHVPVLESEDEDEDGLPIPKGKSSEVENASGEKMVVDNDEQGSNKKRKAKAA
                                                                                                                                                             DDED-----
                                                                                                                                                                                                                                         GNQ-NLVLGTLSTENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYKTPNIEPQGYSEEEE
                      NSGNALESHNKAK 240
                                                                           KAKVAV-----TPQKTDEKKKG-----
                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                     12.8%; Score 164; DB 10; 26.5%; Pred. No. 0.00012;
                                                                                                                                --PTPK-----KPASSKKRANETTPKAPVS----AK
                                                                                                                                                           ------DYEHDEDDSDGIDVGESEEDDSCEYDSEEDE
                                                                                                                                                                                                                                                                                                                        33; Mismatches
                                                                           GKAANQSPKSASQV----SCGSCK----KTF
                                                                                                                                                                                                                ----PVEFTVTGDRSIHLSGFLEYYQ
                                                                                                                                                                                                                                                                                                                        87;
                                                                                                     - AKQTKKKSQASEGENAK
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                                                                                                     203
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Search completed: May 2, 2002, 22:30:22 Job time: 1583 sec

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Result
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| | 395 a 237 c 296 g 290 t | /db_xref="taxon:3702" | organism="Arabidopsis thaliana" | 11218 | Location/Qualifiers | The Minister of Agriculture and Agri-Food (CA) | Patent: EP 1094112-A 7 25-APR-2001; | Repressing gene expression in plants | Wu,K., Miki,B.L., Tian,L. and Brown,D.C. | 1 (bases 1 to 1218) | Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | Arabidopsis thaliana | thale cress. | | AX139020.1 GI:14274701 | AX139020 | Sequence 7 from Patent EP1094112. | AX139020 1218 bp DNA linear PAT 30-MAY-2001 | | |

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Query Match Best Local

Similarity

90.3**%**; 99.5**%**;

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Submitted (22-OCT-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Paio Alto, CA 9430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e-mail for correspondence: arab@sequence.stanford.edu
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                                                                                                      /translation="MEEMGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLS
VTVGGAKLVIGTLSQOKFPQISFDLVFFOKEFELSHSKATKAVHFIGYKSVHIEQDDFT
SSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKTKAVHFPEPINKKPPESVESKE
DDEDESEEDDDSEKGMDVDEDDSDDDEEEDSEDEEEETPKKPEPINKKRPNESVSKT
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75. .995
                                                                                                                                                                                                                             /product="histone deacetylase-like
/protein_id="AAL24375.1"
/db_xref="GI:16649047"
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Structural analysis of Arabidopsis thaliana chromosome 5. I Sequence features of the regions of 1,044,062 bp covered by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-MDJ22
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CGR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.

S Location/Qualifiers

1 77163

1 177163
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ECLLSSLEEVE I KNK I SVDDGALEVARY FVENSVNI OKVYLRI ASSFLRRGNOAVLKD
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.32091,32233.
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Matches 414;
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2E 1 (bases 1 to 977)

RS Yamada, K., Banh, J., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Sakin, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Full Length cDNA of gene At3g44750 (GI:15230496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agaaagaagactcqaattgcaaaccaaaaa 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Yamada,K., Bahh,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Onodera,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94/710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki.M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                         Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
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                                                                 /note-"This clone is in a modified pBluescript vector
(Lambda ZAP) as a XhoI/SstI insert.
ecotype: Columbia"
1..977
/gene="At3g44750"
1, .62
                                                                                                                                                                                   /organism-"Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="3"
/clone="RAFL06-70-K17 (R11479)"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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histone deacetylase (At3g44750) mRNA,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                       1 (bases 1 to 914)
Wu, K., Tian, L., Malik, K., Brown, D.
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Arabidopsis thaliana
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/protein_id="AAL38837.1"
/db_xref="GI:17529220"
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Pred. No. 5.4e-27;
0; Mismatches 158;
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2 (bases 1 to 914)
Wu,K., Tian,L., Malik,K., Brown,D. and Miki,B.
Direct Submission
Submitted (18-OCT-1999) Pastern Cereal and Oilseed Research
Submitted (18-OCT-1999) Canada, Ottawa, Ontario KIA 0C6, C
Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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EEPTEKKPASSKKRANETTPKAPVSAKKAKVAVTPQKTDEKKKGGKAANQSPKSASQV
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171 c 230 q 232 t
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/protein_id-"AAG28472.1"
/db_xref="Gi:11066135"
/translation-"MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPL
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/cultivar="Columbia"
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/clone="211N2"
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                                        Direct Submission
Submitted (13-APR-2000) Microbiology, University
Fritz-Pregl-Str. 3, Innsbruck 6020, Austria
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Oryza sativa putative histone deacetylase HD2 mRNA, AF255711
AF255711.1 GI:7804959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosidae; eurosids II; Brassicales; Brassicaceae; 1 (bases 1 to 939)
Wu,K., Miki,B.L., Tian,L. and Brown,D.C.
                                                                                                                2 (bases 1 to 894)
Dangl, M., Haas, H., Loidl, P. and Lusser, A.
                                                                                                                                                                 plants
                                                                                                                                                                                  1 (bases 1 to 894)
Dangl,M., Brosch,G., Haas,H.,
Molecular characterization of
                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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/db_xref-"taxon:3702"
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/organism-"Oryza sativa"
/db_xref="dbEST:D15380"
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Pred. No. 2.7e-26;
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                                                 gatgaagatgactcagatgatgacgaggaggaaggattctgaggatgaagaagaggagga
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tetectgtgaatgetaaccagageeccaagte
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/protein_id="AAF70196.1"
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SAEDDSQDEDLSFEDDDDDSSEDDSSEDDEDESDEETFKKPETGKRKVAEIVLKTPS
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Pred. No. 5.5e-24;
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                         ggtaccaaagcaaatgttcatttcattggctacaaatcccccaacatcgagcaggatgac 360
                                                                                 AAGAACCCACACATACAATTTGATCTGATTTTCGATAAAGAGTTTGAGCTGTCGCACACA 237
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Zea mays histone deacetylase

AF254073

AF254073.1 GI:7716949
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Innsbruck, Fritz-Pregl Str. 3/II, Innsbruck 6020,
Location/Qualifiers
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/product="histone deacetylase 2 isoform c"
/protein_id="Asf88625.1"
/protein_id="Asf88625.1"
/db_xref="GI:7716950"
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LDSEDEDELLWYPAVENGKALEKKOKSGEKAVAAPSKSSPDSKKSKDDDDSDEDETD
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DSDEDETDDSDEGLSPEEGDDDSSDEDDTSDDEEEDTFPKKPEVGKKRAAESSVLKT
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188 c 238 g 197
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/db_xref="taxon:4577"
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                                                   gcggtaccaaacgtccatttcatttgcctacaaatcccccaacatcgagcagga--
                                                                                                                                    ATGCCATTGTGTCTGTCAAAATTGATGATAAGAAACTAGTGCTTGGGAACCTTATCAGTTG
                                                                                                                                                                                                          aagacagccttgtccacatttctcaggcttcacttgactgcacagtgaaatctggagaat 178
                                     ATTCAAAGACAGCTAGTGTTTTCTTCTGTGGCTACAAGTCACCTGTTCCTCTGTTTGAGT
                                                                                    AGAAGCATCCTCAAATCTCTTGTGATCTGGTATTTGATAAAGATTTTGAGTTATCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
AR168371
                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1307)
Haldwin,D.Adelphi., Briggs,S.P. and Crane,V.
Maize histone deacetylases and their use
Patent: US 6287843-A 17 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
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17
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1. .1307
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260 c 308 g
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                                                                                                                                                                                                                                                                                               Score 112;
Pred. No. 6.
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Best Local Sim
Matches 362;
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                                                                                                                                                                         ttcactagttcggatgatgatgatgttcctgaagctgttcctgctcctgcccctactg--
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tctgatgatgaagatga-
                               AAATCAAGTCCGGATTCCAAGAAGAGCAAGGATGACGATGATTCTGATGAGGACGAGACT 539
                                                         gccaaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgag
                                                                                         AATGGCAAAGCTGATGGGAAGAAACAGAAAAGTCAAGAAAAGGCAGTTGCTGCACCTTCA 479
                                                                                                                     -ctgttactgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaag
                                                                                                                                                      GAAATGGATCTTGATTCTGAAGATGAAGACGAGGAGCTGAATGTTCCAGTAGTCAAGGAA 419
                                                                                                                                                                                                                TCAMAAACTACCAGCGTCTTCTTCACTGGCTACAAGGTTGAACAGCCATTCGAGGAAGAT 359
                                                                                                                                                                                                                                                                                                                                    GCCTTGATGTATGTCAAAATTGATGATCAGAAACTTGCCATTGGAACCCTCTCTGTTGAC
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AR168369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1191)
Baldwin,D.Adelphi., Briggs,S.P. and Crane,V.C.
Maize histone deacetylases and their use
Patent: US 6287843-A 13 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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             gttactgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaaggcc
                                                         gatgatgatgattcctgaagctgttcctgctcctg------
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                                                                                                           aatgttcatttcattggctacaaatcccccaacatcgagcaggatgacttcactagttcg
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                                                                                        AGTGTATTTTTCTCTGGTTACAAGGTTGAGCAGCCAATTGAGGGAGATGAAATGGATCTT
                                            GATTCTGAGGATGAAGAGGAGGAGCTAAACATTCCAGTAATCAAGGAAAATGGCAAAGCT
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Sequence 15
AR168370
AR168370.1
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Unknown.
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Baldwin,D.Adelphi., Briggs,S.P. and C
Maize histone deacetylases and their
Patent: US 6287843-A 15 11-SEP-2001:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified
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patent US 62
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Pred. No. 1e-15;
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                                                                     ggtaccaaagcaaatgttcatttcattggctacaaatcccccaacatcgaqcaggatgac 360
                                                                                                            AAGAACCCACACATACAATTTGATCTGATTTTCGATAAAGAGTTTGAGCTGTCGCACACA 315
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Baldwin,D.Adelphi. Briggs,S.P. and Crane,V.C.
Maize histone deacetylases and their use
Patent: US 6287843-A 11 11-SEP-2001;
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U82815.1
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Submitted (09-JAN-1997) Department of Microbiology, University
Innsbruck, Fritz Pregi-Strasse 3, Innsbruck 6020, Austria
Location/Qualifiers
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Science 277 (5322), 88-9
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/protein_id="AAB63262.1"
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Search completed: May 2, 2002, 20:14:50 Job time: 15504 sec

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Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argenthe, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L., and Hanson, D. Arabidopsis thaliana Gene Expression MicroArray Uppublished (1999)

Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
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9
                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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with a PCR product of the target gene."
a 141 c 132 g 192 t 25 others
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                                                                                                                                    4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
                                                                                                                                                                               Email: service@genomesystems.com
Location/Qualiflers
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EST 06-SEP-2000

linear

mRNA

426 bp

AV539421/c LOCUS

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Eukaryotta; Viridiplandae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplandae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 426)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Alarge scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                   Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Locatlon/Qualifiers
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/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoR; Site_2:
AV539421 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clone R2131f01F 3', mRNA sequence.
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Kazusa DNA Research Institute
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100.0%; Pred. No. 3.4e-50;
tive 0; Mismatches 0;
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/strain="Columbia"
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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                    /strain-"Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 1.1e-57;
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    483
    organism-"Arabidopsis thaliana"

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Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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701931423 A. thaliana, mixed source Arabidopsis thaliana cDNA clone
501931423, mRNA sequence.
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Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gililland,D.,
Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
                                                                                                                                                                                                                               /clone-"SQ233q03F"
/clone_lb-"Arabidopsis thaliana green siliques Columbia"
/tisaue_type-"green siliques"
/note-"Vector: pBluescriptil SK-; Site_1: EcoR1; Site_2:
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids 11; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 475.4; DB 9;
Pred. No. 4.4e-57;
0; Mismatches 1;
                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                              157
                                                                                                                                                                                      /strain="Columbia"
/db_xref="taxon:3702"
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Arabidopsis thallana
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:

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1 (bases 1 to 503)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 morredundant expressed sequence tags from normalized and size selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu(ekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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AV542413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957 caagggcaagggaaagggtagagcttaaggacgtggatcaaggagagaggttttgggttttc 1016
                                                    658 g-ctcttaagaagcctgagccaatcaacaagaagaggccaaatgaatctgtatccaaaac 716
                                                                                                                                                                                                                                                                  968
                                                                                                                                                                                                                                                                                  897 caacaagaagccattcaactcaggcaaacaatttggtggttccaacaagaggttctaa 956
                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                                                                                                                                                       193 CAAGGGCAAGGGAAAGGTAGAGGTTAAGGACGTGGATCAAGGAGGAGGTTTTGGGTTTT 134
493 GACTCCTAAGAAGCCTGAGCCAATCAACAAGAAGAGGCCAAATGAATCTGTATCCAAAAC 434
                                                                                                                                                          433 ACCCGTCTCTGGAAAGAAGNNNNNNNNNNNNNNNNNNNNTTCTACTCCTCAGAAGAC 374
                                                                                                                                                                                                                                                                                                                                                     717 acceptetetggaaagaaageaaaaceageageageaceagettetaeteeteagaagae
                                                                                                                                                                                                                                                                837 gtctcctgtgaatgctaaccagagccccaagtctggaggtcaatcatccgytggtaacaa
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/clone="R2183f11F" /clone_lib="Arabidopsis thaliana roots Columbia" /tissue_type="roots"

/db_xref="taxon:3702"

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Eukaryota; thaliana Eukaryota; Embryophyta; Tracheophyta; Spranatophyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spranatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 483)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana; Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                Length 503;
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                                                                            41.2%; Score 502; DB 9; I
100.0%; Pred. No. 8.7e-61;
tive 0; Mismatches 0;
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AV559263.1 GI:8730689
                                                                                            Best_Local Similarity 100.0
Matches 502; Conservative
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
20363093
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                            AV543549 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clone RZ202e12F 3', mRNA sequence.
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/clone=lib-"Rabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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1142 atgaatatttgctgaaatgagaaagaagactcgaattgcaaac 1184
                  Score 534.8; DB 9;
Pred. No. 2.3e-65;
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98.6%;
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/clone_lib="A. thallana, Columbia Col-0, rosette-2"
/tissue_type="rosette"
/tissue_type="rosette"
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library was derived from untreated rosette tissue from
Arabidopsis thallana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat mossyvermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. CDNA synthesis was initiated
using a Not1-oligo(dT) primer. Pouble-stranded CDNA was
blunted, lighted to Sal1 adaptors, digested with Not1.
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(bases 1 to 552)

Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Grorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nqyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carplo, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Eider, L. and Hanson, D.

Arabidopsis thallana Gene Expression MicroArray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                          198 ACGTGGATCAAGGAGAGAGGTTTTTCGAGTAGATGAAAAACACTTGGAAGTGTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 gatgaagatgactcagatgatgacgaggaaggaaggattctgaggatgaagaagaagagga 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701545727 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545727, mRNA sequence.
                                                                                                   138 GTTTTGGATTTTTATCTTATTTAGTATAACTTGTTATCGGATGAGCTATTTTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: David Smoller, Ph.D. Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc. 4633 World Parkway Circle, St. Louis, MO 63134, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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/cultivar="Columbia Col-0"
/db_xref="taxon:3702"
/clone="701545727"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: service@genomesystems.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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134 c 92 g
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Matches 527; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 877-577-2733
Fax: 314-427-3324
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us-09-645-337-7.rst

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                            /tissue_type="mixed leaf and root"
/dev_stage="10-14 day old"
/dev_stage="10-14 day old"
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Site_1: EcoRI; Site_2: EcoRI; AD Arabidopsis thaliana
library enriched for salt-induced transcripts from
wildtype (Col-0 g11) 10-14 day-old seedlings treated with
160 mM Nacl for 4 hours."
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96.1%;
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Best Local S.
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EST 06-SEP-2000

AV543093 AV543093 584 bp mRNA linear EST 06-SEP-200 AV543093 Arabidopsis thaliana roots Columbia Arabidopsis thaliana CDNA clone R2196b09F 3', mRNA sequence. AV543093

DEFINITION AV543093/c

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ACCESSION

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1 (bases 1 to 584)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-rendant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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                                                                                                                                                                                                                                                                                            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                  Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                            The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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/organism-"Arabidopsis thallana"
/strain-"Columbia"
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 AV543093.1 GI:8704853
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TITLE
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COMMENT
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VERSION
KEYWORDS
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May 2, 2002, 18:43:44 ; Search time 3265.32 Seconds (without alignments) 5034.512 Million cell updates/sec
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AV442939 AV542939
T45874 9137 Lambda
AA597939 29188 Lam
AV37871 AV537871
AV541169 AV541169
AV550412 AV550412
AV551556 AV551556
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AV543549 AV543549
AI998449 701545727
AV542413 AV542413
AV559263 AV559263
AV565954 AV565954
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AV539421 AV539421
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1218
1 gtctttcgcttctaaaaaaa......aaaaaaaaaaggcggcgc 1218
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                        13736207 seqs, 6748477542 residues
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Maximum Match 100%
Listing first 45 summaries
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9 AV54249
9 AV542413
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AV537871
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Match Length DB
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411.4
409.4
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                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                   Sequence:
                                                                                                                                                                                          Searched:
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| C99809 C99809 YAC AA713170 32730 Lam AV539161 AV539161 AV539161 AV539161 AV539161 AA395217 Z7000 Lam AV3939637 AV539637 Z35338 ATTS3723 A Z35338 ATTS3723 A Z35338 ATTS3723 A Z35337 ATTS3723 A Z35337 ATTS3723 A Z35337 ATTS3723 A Z37505 ATTS3039 AC Z24526 ATTS968 Ral Z17565 ATTS0396 AC A1955198 701502609 BF2770501 GA_EB003 BF2770701 GA_ | | mRNA linear EST 17-MAY-2001) library enriched for y seedlings; 4h 160mM Nacl stress 01A07 similar to (AF044914) sequence. | thale cress. Arabidopsis thaliana Arabidopsis thaliana Arabidopsis y Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudloctyledons; core eudlocts; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | D., Kor | egulated in salt overly sensitive (2001) | | gil" gil" a (Col-0 gil) library enriched |
|--|----------------------|--|--|--|--|---|--|
| 10 C99809 9 AA713170 9 AV513170 9 AV5499161 9 AV549917 9 AV549917 10 Z35338 10 Z35338 10 Z35337 10 Z3537 10 Z35337 10 Z35337 10 Z35337 10 Z35337 10 Z35337 10 Z35337 10 Z3537 10 Z3537 | ALIGNMENTS | DEE44690 AT AD A. thallana (Col-0 gll) library ent ADD1A077 AD A. thallana (Col-0 gll) library ent Salt induced transcripts; 10-14 day seedlings; 4 Arabidopsis thallana cDNA clone AD01A07 similar putative histone deacetylase, mRNA sequence. BE844690. GI:10277068 | na Lantae; Streptopi noliophyta; eudi II; Brassicales; | Cushman,M.A., Ru 1,J., Cushman,J.C | stress r 363-375 | cenistry da (57-0014, USAcdu | Location/Qualiflers Location/Qualiflers 1 728 /organism-"Arabidopsis thaliana" /strain-"ccctype Columbia gll" /clone-"Ab01A07" /clone_lib-"AD A. thaliana (Col-0 |
| 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | | BE644690 AALLANDAOTA AA. thallan SALLINDUCA A. thallan Arabidopsis thaliana cD putativo histone deacet BE844690 GI:10277068 | thale cress. thale cress. thaliana Eukaryota; Viridipla Spermatophyta; Magno Rosidae; eurosids II | <pre>1 (bases 1 to 728) Gong.Z., Koiwa,H., Cushm Matsumoto,T.K., Zhu,J., ,P.M.</pre> | nat are uniquel tants ysiol. 126 (1) | Contact: Cushman JC Department of Biochemistry University of Newada MS200, Reno, NV 89557-0014 Tel: 775-784-1918 Fax: 775-784-1650 Email: jcushman@unr.edu Elate: AD01 row: A colum | Location/C 1.728 /organism/strain-ic/db_xref-ic/clone-"AL/Clone- |
| 363.4 29.8 354.6 29.1 37.7 26.8 8 3.7 26.8 8 22.0 22.0 22.0 22.0 22.0 22.0 22.0 | | BEB44690 AD01A07T Salt-indi Arabidop putative BE844690 | EST. thale cr Arabidop Eukaryot Spermatc | 1 (base Gong.Z., Matsumot ,P.M. | Genes that are (sos) mutants Plant Physiol. 21249177 | Contact: Departmc Universi MS200, B Tel: 775 Fax: 775 Email: j Plate: | POLYA-NO. POLYA-NO. LO 1. 70 70 70 70 70 70 70 70 70 70 70 70 70 |
| 0 00 00 00 00 00 00 00 00 00 00 00 00 0 | RESULT 1 BE844690 | LOCUS DEFINITION ACCESSION VERSION | KEIWOKUS SOURCE ORGANISM | REFERENCE AUTHORS | TITLE JOURNAL MEDLINE | COMMENT | FEATURES Source |
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571 tgactcttgagaa-aggaatggatggttgatgaagatgactcagatgatgacgaggagga 629 | 1111 | 1 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
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                                                                                21036 GTTGACAAGGATGACAATGACAATAAGGATGATGAGGAGGAGGAGGAGGAGACAGATGAGGAG 20977
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4.0%; Score 48.8; DB 4; Length 32207;
Best Local Similarity 61.5%; Pred. No. 0.015;
Matches 128; Conservative 0; Mismatches 77; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Red-Amn, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
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1185 Avenue of the Americas
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Patent No. 6183751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 4518:
TELECOMUNICATION INFORMATION:
TELEFHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LEWGTH: 32207 base pairs
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ATTORNEY/AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
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COMPUTER READABLE FORM:
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STATE: New York
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US-08-757-669A-20/c
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Search completed: May 2, 2002, 20:16:07 Job time: 15154 sec

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                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.1%; Score 49.6; DB 2; Length 3581; Best Local Similarity 65.2%; Pred. No. 0.0041; Matches 73; Conservative 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Gelman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: Envery From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/728,323A
           TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: Osteoblastic cell line MC3T3E1
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STREET: 1185 Avenue of the Americas
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base_pairs
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IBM PC compatible
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EDNESS: single
single
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COMPUTER READABLE FORM:
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LOCATION: 284..2671
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STATE: New York
COUNTRY: U.S.A.
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; LOCATION: 1..3
US-08-728-323A-1
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF NUMBER OF SEQUENCES: 20
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Ouery Match 4.0%; Score 48.8; DB 2; Length 3489; Best Local Similarity 61.5%; Pred. No. 0.0064; Matches 128; Conservative 0; Mismatches 77; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08770379; Patent No. 2849564
GENERAL INFORMATION:
GENERAL APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: MOOFE, Patrick S.
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
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TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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US-08-770-379-20/c
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COMPUTER READABLE FORM:

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US-08-738-349-1
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Patent No. 6124100
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
FILE REFERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278
EARLIER PILING DATE: 196-02-26
NUMBER OF SEQ 1D NOS: 3
SOFTWARE: WordPerfect 6.1/Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1055 tittitatottatittattagtataacttgttatoggatgagctattttgagtatttgcaa 1114
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4.1%; Score 50; DB 1; Length 5852;
Best Local Similarity 57.8%; Pred. No. 0.0039;
Matches 89; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Indels
         COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                  NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 2378..5038
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; ORGANISM: human
US-09-253-691-3
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US-07-867-106-2
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LENGTH: 397
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425 ctgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaaggccaaac 484
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0
    Length 397;
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APPLICANT: Takeshita, Makoto
APPLICANT: Rawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
GORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
Query Match 4.1%; Score 49.8; DB 3; Length 3° Best Local Similarity 49.8%; Pred. No. 0.0016; Matches 126; Conservative 0; Mismatches 127; Indels
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COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
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APPLICATION NUMBER: US 08/364,439
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Patent No. 5869638
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REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02.
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STREET: 1300 I Street, N.W.
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APPLICATION NUMBER: US 08
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3581 base pairs
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COMPUTER READABLE FORM:
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614 atgatgacgaggaaggaattetgaggatgaagaagaagaaggaggaggetettaagaageetg 673
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith I,
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52.8; DB 2; Length 966;
Pred. No. 0.0004;
0; Mismatches 164; Indels
                                                                                                                                                                                          PF-0177 US
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    US/08/766,738
                                                                                                                                            NAME: BIILINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/FOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.38;
                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US
FILING DATE: Herewith
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                     FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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                                                                                 APPLICATION NUMBER:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY: Conser; CLONE: 1813361
US-08-766-738-2
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                                                                                                                                       APPLICANT: Tureci, Ozlem
APPLICANT: Tureci, Ozlem
APPLICANT: Sakin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Pfreundschuh, Michael
TTILE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And US
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
CURRENT APPLICATION UNMBER: US/09/590,113
CURRENT FILING DATE: 2000-06-08
PRIOR FILING DATE: 1998-10-22
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Patent No. 5916749
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
NUMBER OF SEQUENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57.8; DB 4; Length 12
Pred. No. 2.5e-05;
0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: USS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                           US-09-590-113-2
; Sequence 2, Application US/09590113
; Patent No. 6306389
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613 gatgatgacgaggaagga 633
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51.3%;
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Best Local Similarity 51.34
Matches 134; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
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US-09-411-812A-2
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APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins,
TITLE OF INVENTION: Thereof
FILE REFERENCE: LUD 5525
CURRENT APPLICATION NUMBER: US/09/177,325B
CURRENT FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 15
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                            NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                                                                                                                         INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLGGY: linear INMEDIATE SOURCE:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
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                                                                                             TELEPHONE: (703)836-930
TELEFAX: (703)683-4109
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                                                                                                                                                                                                                                                 US-08-232-463-14
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LENGTH: 1276
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APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, A
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: LUD 5525.1 CIP
CURRENT APPLICATION NUMBER: US/09/411,812A
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 09/177,325
PRIOR APPLICATION NUMBER: 1998-10-22
NUMBER OF SEQ ID NOS: 14
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  Length 1276;
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Query Match 4.7%; Score 57.8; DB 4; Length 1
Best Local Similarity 51.3%; Pred. No. 2.5e-05;
Matches 134; Conservative 0; Mismatches 127; Indels
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Pred. No. 2.5e-05;
0; Mismatches 127; Indels
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Best Local Similarity 51.3%;
Matches 134; Conservative
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases and Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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Patent No. 6287843
GENERAL INFORMATION:
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US-09-282-305-11
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NAME/KEY: CDS
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LENGTH: 1283
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Matches 359;
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463 Patent No. 5670367
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STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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CLASSIFICATION: 435
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51.4%; Pred. No. 1.1e-18;
ive 0; Mismatches 329; Indels 13;
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APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION UNMBER: US/09/282,305
CURRENT FILING DATE: 1999-04-03
PRIOR APPLICATION NUMBER: 60/080,563
WUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                  524 acgaggaagatgagtctgatgatgaagatgaagtctgaagag 565
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Patent No. 6287843
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Best Local Similarity 51.49
Matches 362; Conservative
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US-09-282-305-13
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ORGANISM: Zea mays
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                               478 gecaaaccigeegaagigaageeigeagaagaagaageeigaaicagaegaggaagaigag
                                                   GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TILLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR PILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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9.1%; Score 111.2; DB 4; Length 1245;
Best Local Similarity 51.6%; Pred. No. 1.4e-18;
Matches 430; Conservative 0; Mismatches 363; Indels 41;
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Patent No. 6287843
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US-09-282-305-15
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LENGTH: 1245
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OM nucleic - nucleic search, using sw model

May 2, 2002, 20:15:18 ; Search time 100.71 Seconds (without alignments) 2970.724 Million cell updates/sec Run on:

US-09-645-337-7 1218 1 gtctttcgcttctaaaaaaa.....aaaaaaaaaaagggcggccgc 1218 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

383533 seqs, 122816752 residues Searched: 767066 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Result No. | Score | Query Match | Length | DB | ID | Description |
| - | 112 | 9.2 | 1307 | 4 | US-09-282-305-17 | Sequence 17, Appl |
| 7 | 111,6 | 9.5 | 1191 | 4 | US-09-282-305-13 | 13, |
| 3 | 111.2 | 9.1 | 1245 | 4 | US-09-282-305-15 | 15, |
| 4 | 111.2 | 9.1 | 1283 | 4 | US-09-282-305-11 | Sequence 11, Appl |
| c 2 | 85.4 | 7.0 | 7218 | - | US-08-232-463-14 | 14, |
| 9 | 57.8 | 4.7 | 1276 | 4 | US-09-177-325-2 | |
| 7 | 57.8 | 4.7 | 1276 | 4 | US-09-411-812A-2 | 7 |
| 80 | 57.8 | 4.7 | 1276 | 4 | US-09-590-113-2 | 'n |
| 6 | 52.8 | 4.3 | 996 | 7 | US-08-766-738-2 | Sequence 2, Appli |
| c 10 | 20 | 4.1 | 5852 | - | US-07-867-106-2 | 'n |
| c 11 | 49.8 | 4.1 | 397 | ٣ | US-09-253-691-3 | Sequence 3, Appli |
| 12 | 49.6 | 4.1 | 3581 | ~ | US-08-738-349-1 | 7 |
| 13 | 48.8 | 0.4 | 3489 | ~ | US-08-728-323A-1 | H |
| - | 48.8 | 4.0 | 32207 | ~ | US-08-770-379-20 | 20 |
| - | 48.8 | 0.4 | 32207 | 4 | US-08-757-669A-20 | 50 |
| c 16 | 48.8 | 4.0 | 32207 | 4 | US-09-230-371A-20 | 20 |
| 17 | 48.6 | 0.4 | 1223 | m | US-09-154-874-4 | Sequence 4, Appli |
| 18 | 47.6 | 3.9 | 2625 | 4 | US-09-245-041-18 | 18 |
| c 19 | 47 | 3.9 | 509 | 4 | US-09-030-607-202 | 202, |
| | 47 | 3.9 | 509 | 4 | US-09-439-313-202 | |
| c 21 | 46.6 | 3.8 | 470 | 4 | US-09-020-956-102 | 102, |
| | 46.6 | 3.8 | 470 | 4 | US-09-030-607-102 | 102, |
| c 23 | 46.6 | 3.8 | 470 | 4 | US-09-439-313-102 | 102, |
| 24 | 46.6 | 3.8 | 2277 | - | US-08-676-967-2 | Sequence 2, Appli |
| 25 | 46.6 | 3.8 | 2277 | - | US-08-676-974-2 | Sequence 2, Appli |
| 26 | 46.6 | 3.8 | 2277 | ~ | US-09-098-487-2 | 7 |
| 27 | 46.2 | 3.8 | 2295 | - | US-08-375-300-3 | Sequence 3, Appli |

| Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 193, Appl Sequence 191, Appl Sequence 191, Appl Sequence 181, Appl Sequence 187, Appl Sequence 187, Appl Sequence 187, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli |
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| US-09-177-431-3 PCT-US95-16930-3 US-08-375-3300-1 US-09-375-3300-1 US-09-461-697-193 US-09-461-697-1991 US-09-461-697-187 |
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ALIGNMENTS

| RESULT 1 US-09-282-305-17 Sequence 17, Application US/09282305 Sequence 17, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44 CURRENT PAPLICATION NUMBER: 60/080,563 PRIOR PPLICATION NUMBER: 60/080,563 PRIOR PPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1999-04-03 PRIOR FILING DATE: 1999-04-03 SOGTWARE: Patentin Ver. 2.0 SEQ ID NO. 17 LENGTH: 1307 TYPE: DNA COGANISM: Zea mays FRATURE: NAME/REY: CDS US-09-282-305-17 US-09-282-305-17 | Ouery Match Best Local Similarity 54.0%; Fred. No. 8.7e-19; Matches 282; Conservative 0; Mismatches 225; Indels 15; Gaps Oy 59 caatggagtctgggggggggggggggggggggggggggg |
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990S-0161406-
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| 20-JUL-19 21-JUL-19 21-JUL-19 | 21-JUL-1 22-JUL-1 | 22-JUL-1 | 22-JUL-1 | 23-JUL-1 | 23-JUL-1 | 26-JUL-1 | 27-JUL-1 | 27-JUL-1 | 27-JUL-1 | 28-30L-1 | 02-AUG-1 | 02-AUG-1 | 03-AUG-1 | 04 - AUG - 1 | 04 - AUG - 1 | 05-4116-1 | 06-AUG-1 | 06-AUG-1 | 09-AUG-1 | 09-AUG-1 | 10-AUG-1 | 12-AUG-1 | 13-AUG-1 | 13-AUG-1 | 16-AUG-1 | 17-AUG-1 | 20-AUG-1 | 20-AUG-1 | 20-AUG-1 | 23-AUG-1 | 23-AUG-1 | 25-AUG-1 | 27 - AUG - 1 | 27 - AUG - 1 | 27-AUG-1 | 30-AUG-1 | 01-SEP-1 | 07-SEP-1 | 10-SEP-] | 13-SEP-1 | 15-SEP-1 | 20-SEP- | 22-SEP- | 23-SEP- | 24 - SEP- | 28 - SEP - 3 | 29-5EP- | 05-0CT-1 | 06-OCT-1 | 07-0CT-1 | 08-0CT-1 | 13-OCT-1 | 13 OCT - 1 | 13-0CT-1 | 14 -OCT-1 | - E-0-1 |
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99US-0144814.
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99US-0145145.
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Pred. No. 1.5e-15;
0; Mismatches 6; Indels
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        990S - 0159330
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Matches 114; Conservative
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28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
14 - OCT - 1999;
18 - OCT - 1999;
21 - OCT - 1999;
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22 - OCT - 1999;
22 - OCT - 1999;
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05 - MAR - 1999;
23 - MAR - 1999;
25 - MAR - 1999;
25 - MAR - 1999;
01 - APR - 1999;
06 - APR - 1999;
16 - APR - 1999;
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                                                                                                                                                                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 72846.
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05-MAR-1999;
03-MAR-1999;
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25-MAR-1999;
01-ARR-1999;
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PR 16-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130407.

PR 23-APR-1999; 99US-0130419.

PR 23-APR-1999; 99US-0130419.

PR 28-APR-1999; 99US-013248.

PR 28-APR-1999; 99US-013248.

PR 30-APR-1999; 99US-013248.

PR 04-MAY-1999; 99US-0132486.

PR 04-MAY-1999; 99US-0132486.

PR 11-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0134286.

PR 12-MAY-1999; 99US-013462.

PR 21-MAY-1999; 99US-013452.

PR 18-UNN-1999; 99US-013945.

PR 21-MAY-1999; 99US-013945.

PR 21-MAY-1999; 99US-013945.

PR 21-MAY-1999; 99US-013945.

PR 18-UNN-1999; 99US-013945.

PR 21-UNN-1999; 99US-0
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deacetylase genes, used for producing transgenic plants which have increased disease resistance

Claim 1; Page 77-79; 87pp; English.

The present sequence encodes a maize histone deacetylase. This DNA belongs to family 2, ZmHD2 and appears to affect chromatin structure at promoters of RNA polymerase I and thus regulate ribosomal RNA production. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.

Sequence 1245 BP; 385 A; 250 C; 324 G; 286 T; 0 other;

9 711 caaaacacccgtctctggaaagaaggcaaaaccagcagcaccagcttctactcctca 770 ggagttgcggtgacaccaaaaaacgctactaaggtgactcctgaagaagacagccttgtc 132 ggtctcgaggtcaaacctggatccactgtcaagtgtgagcctggacatggctttatcctg 155 cacatttctcaggcttcacttgactgcacagtgaaatctggagaatctgtggttttgagt 192 attagetttgattttggtttttgataaagagtttgagetttcacacageggtaccaaagea 312 aatgitcaittcaitggctacaaatcccccaacaicgagcaggaigacttcactagitcg 372 gatgatgaggatgttcctgaagctgttcctgctcctg-------cccctactgct 420 gattetgaggatgaagaggaggagetaaacatteeagtaateaaggaaaatggeaaaget 452 gttactgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaaggcc 480 13 taaaaaaaaaacctaaccacctctctctctctcctcgttcaacaacaatggagttctgg 72 Gaps agigiatititiciciqqitacaaggitgagcagccaatigagggagatgaaaiggaicti ---gqttgatgaagatgactcagatgatgacgaggaggaaggattctgaggatgaagaag 156 cacqtttcccaggctgcccttgggggaatcaaagaaaagt...gacagtgccttaatgtat gatgggaaggaggagcagaaaaatcaagaaaggcagtagctgctacagcttcaaaatca aaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgagtct 513 agtettggeettgaaaagaaaageaaggatgaetetgatgattetgatgaggatgagtet gatgattctgatga----ggatgattctgatgattctgatgaaggcgagggattatctcc aaccccaactcctaaaaagccagaggca---ggcaagaagagaggtgctgaaaatgctct aggaggagetettaagaageetgageeaateaacaagaagaggeeaaatgaatetgtate DB 20; Length 1245; gatgatgaagatgaagtctgaagaggatgatgactcttgagaaaggaatggat Indels Pred. No. 1.5e-15; 0; Mismatches 363; Score 111.2; 9.18; 51.6%; Best Local Similarity 51.6 Matches 430; Conservative Query Match 213 313 333 453 573 73 96 133 193 253 373 393 421 481 594 651 ò Q q g 9 a q qq g g qq q 셤 ò ò ò ò ò ò ò ò ò ò ò ò

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0; Mismatches 328; Indels

Matches

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121 gacageottgtccacatttctcaggettcacttgactgcacagtgaaatetggagaatet 180

RNA polymerase 1; ribosomal RNA production; promoter regulator; promoter; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity; The present sequence encodes a maize histone deacetylase. This DNA belongs to family 2, ZmHDZ and appears to affect chromatin structure at promoters of RNA polymerase I and thus regulate ribosomal RNA production. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase. used for producing transgenic plants which have Maize histone deacetylase; family 2, ZmHD2; chromatin structure; Length 1283; gaagacagaagaagaagaaagaaggagacacaccgccacacaccccagctaa Sequence 1283 BP; 383 A; 259 C; 333 G; 308 T; 0 other; "Maize histone deacetylase" DB 20; .5e-15; Score 111.2; Pred. No. 1. Location/Qualifiers 38..1336 Claim 1; Page 70-72; 87pp; English. VC; (PION-) PIONEER HI-BRED INT INC. BP Maize histone deacetylase-6 DNA Crane disease response promoter; ds. 9.1%; AAX90842 standard; DNA; 1283 disease resistance 98US-0080563. 99WO-US07370 (first entry) /product-Local Similarity 50.7 nes 359; Conservative Baldwin DA, Briggs SP, /*tagdeacetylase genes, WPI; 1999-611038/52. P-PSDB; AAY28802. 13-JAN-2000 W09951731-A2 02-APR-1999; 03-APR-1998; Zea mays. Query Match 771 AAX90842 g à

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Pred. No. 1.2e-15;
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                                  AAX90843 standard; DNA; 1191 BP
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Best Local Similarity 51.4%;
Matches 362; Conservative (
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RNA polymerase I; ribosomal RNA production; promoter regulator; promoter; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening; pathogenicity;
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RNA polymerase 1; ribosomal RNA production; promoter regulator; promoter;
transcription; plant transformation; heterochromatin; disease resistance;
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0; Mismatches 127;
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Watches 239;
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The present sequence encodes a maize histone deacetylase . This DNA belongs to family 2, ZmHD2 and appears to affect chromatin structure at promoters of RNA polymerase I and thus regulate ribosomal RNA production. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
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Pred. No. 9.9e-16;
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                                                                                                                                                                                                                                                                                                      Claim 1; Page 80-82; 87pp; English.
                                                                                                                                                     Crane VC
                                                                                                              (PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                       WPI; 1999-611038/52
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14-0CT-1999
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Matches 282;
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| 06-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 10-JUN-1999; 10-JUN-1999; 10-JUN-1999; 118-JUL-1999; 118 | JUL |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                      Histone deacetylase; AtHDA2A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation; ds.
302 cttgggggaaaggaagtgtttactttgttggatacaaaactcccaacattgagccacaag 361
                               359 acttcactagttcggatgatgatgatgttcctgaagctgttcctgctcctgcccctactg 418
                                                   Nucleotide sequence of a histone deacetylase designated AtHDA2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product- "histone deacetylase AtHDA2A"
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Score 156.2; DB 22; Length 939; Pred. No. 9.3e-26;

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Query Match Best Local Similarity

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334 aaatcccccaacatcgagcaggatgacttcactagttcggatgatgaggatgttcctgaa 393
                                                                 214 cttgttattggaacactttcacaagacaagttccctcagattagctttgatttggttttt 273
                                                                                                                                                                                                                     274 gataaagagtttgagctttcacacagcggtaccaaagcaaatgttcatttcattggctac 333
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                                                                                                                                                                                                                                                                                                    325 aaaactcccaacattgagccacaaggctattctgaggaagaagaagaagaagaagaagaa 384
                                                      getactaaggtgactectgaagaagacageettgtecacattteteaggetteaett--- 153
                                                                                                                                     145 gaatgtaaaaacaagaaagggagagtttgtgcctttacatgtaaaggttgggaaccagaac 204
ttetetetteetegtteaacaacgagagttetggggagttgeggtgacaccaaaaae 96
                        tttteteaacettgattettageeatggagttetggggaattgaagttaaateaggaaag
                                                                                                           gactgcacagtgaaatctggagaatctgtggttttgagtgtgactgttggtggggctaaa
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05 - MAR - 1999;
23 - MAR - 1999;
25 - MAR - 1999;
26 - MAR - 1999;
01 - APR - 1999;
06 - APR - 1999;
16 - APR - 1999;
119 - APR - 1999;
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23-APR-1999;
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30-APR-1999;
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06-MAY-1999;
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179 ctgtggttttgagtgtgactgttggtggtgggctaaacttgttattggaacactttcacaag 238
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990S - 0151930 . 990S - 0151930 . 990S - 0151930 . 990S - 0153758 . 990S - 0153758 . 990S - 0153758 . 990S - 0154779 . 990S - 0154779 . 990S - 0154779 . 990S - 0154753 . 990S - 0158029 . 990S - 0158029 . 990S - 0158029 . 990S - 015929 . 990S - 015929 . 990S - 015929 . 990S - 015939 . 990S - 015939 . 990S - 016074 . 990S - 016074 . 990S - 016078 . 990S - 016078 . 990S - 016078 . 990S - 016098 . 990S - 016098 . 990S - 016098 . 990S - 0161405 . 990S - 0161405 . 990S - 0161350 . 990S - 0161392 . 990S - 0161992 .
 01-SEP-1999;

07-SEP-1999;

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                                                            Arabidopsis thaliana
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28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
                                                                                        EP1033405-A2
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10-JUN-1999;
14-JUN-1999;
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17-JUN-1999;
18-JUN-1999;
                                                                                                                     06-SEP-2000
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    ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acttcactagttcggatgatgatgttcctgaagctgttcctgctcctgcccctactg 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 atgaagaggatgagtctgattctgacggaatggatgaaggtgatgatgattctgatggtgaggatt 543
                                                                                                                                                                                                                                                                                                                                                                                                                                          acageettgteeacattteteaggetteactt---gactgeacagtgaaatetggagaat 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgttactgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaagg 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccaaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgagt 538
                                                                                                                                                                                                                                                                                                                                                                                  tggagttctggggagttgcggtgacaccaaaaacgctactaaggtgactcctgaagaag 121
                                                                                                                                                                                                                                                                                                                                                                                                               tggagttctggggaattgaagttaaatcaggaaagccagttacagtgactcctgaagaag 123
                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                     ttttcagctgctcataaaccctaaaaatcctcttttttctcaaccttgattcttagcca 63
                                                                                                                                                                                                                                                                                                                         totttogottotaaaaaaaaacctaacaacctotototototootogttoaacaacaa 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctgtggttttgagtgtgactgttggtggggctaaacttgttattggaacactttcacaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttgtgcctttacatgtaaaggttgggaaccagaacttggttctgggaactctatcgactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acaagttccctcagattagctttgatttggtttttgataaagagtttgagctttcacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgccaaggctgtagctaaaccaaaggctaagcctgcagaagtgaagccagctgttgatg
                                                                                                                                                                                                                                                                 Length 1002;
                                                                                                                                                                                                                                                                               Pred. No. 3.4e-27;
0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                 DB 21;
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                                                                                                                                                                                                                                                                 Score 162.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC45610 standard; DNA; 991 BP.
                                                                                                                                                                                                                                                                13,3%;
57,1%;
99US-0160768.
99US-0160814.
99US-0160814.
99US-0160814.
99US-0160980.
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99US-0161406.
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                                                                                                                                                                                                                                                                               Best Local Similarity 57.1
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctgatgatgaaga 551
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                             64
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ID AAC4
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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| | 99US-0145085 99US-0145087 | Sne | 506 | Sn6 | Sne | SOS | Sn6 | 506 | Sne | Sne | SOC | Sn6 | Sn6 | S06 | Su6 | SDS | 908 | Sne | Sne | Sn6 | Sus | Sus 90s | sn6 | Sne | Sus | Sn6 | SOS | Sn6 | 2008 | Sne | 506 | Suc Suc | Sn6 | Sns | sne | 506 | Sne | Sne | Sn6 | SD6 | Sn6 | Sne | 200 | Sn6 | Sn6 | SDS | Sn6 | Sn6 | Sn6 | S06 | Sne | Sn6 |
|------|------------------------------|--------|--------|-------|----------|-------|-------|------------|-------|----------|-------|------------|------------|-------|------------------|--------|-------|-------|---------|----------|-------|------------|------------|-------|-------|------------|----------|-------|-------|-------|-------|------------|-------|--------|---------|-------|--------|--------------|--------|------------------|--------|--------|-------|-------|--------|-------|-------|-------|-------|-------|-------|----------|
| | 22-JUL-1999; 22-JUL-1999; | :66 | | :66 | :66 | | .66 | 660 | ,66 | :66 | : 55 | ;66 | :66 | , oo | :66 | . 66 | ,66 | :66 | .66 | :66 | . 66. | ,66 ,66 | :66 | 99; | ,66 | 66 | : 5.5 | :66 | .66; | .66 | :66 | . 66 | .66 | 66. | 66; | .66 | :66 | , 66 , 66 | :66 | : 5 5 5 | .66 | :66 | | 66; | .66 | .66 | :66 | | .66 | :66 | | :66 |
| | P.R. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 0.10 | 990S-0132485. | .0-S06 | .0-sne | 0-Sn6 | 0-S06 | 0-S06 | 0-506 | 0-sne | 0-506 | .0-Sn6 | 90S-0 | 0-S06 | 0-506 | o-sne | 0-Sn6 | .0-sne | 0-sne | 0-506 | 0-S06 | .0-Sn6 | 0-S06 | 0-506 | 0-506 | 0-sn6 | 0-S06 | 0-506 | 0-S06 | 0-S06 | 0-506 | 0-506 | 0-506 | 0-S06 | 0-806 | 90s-0. | 0-506 | 0-S06 | .0-Sn6 | .0-Sn6 | .0-S06 | 0-S06 | :0-Sn6 | .0-sne | 0-sne | 0-Sn6 | .0-S06 | 0-sne | 0-S06 | 0-S06 | 90S-0 | 0-806 | 0-506 | 0-806 |
| 0 | 05-MAY-1999; | 99 | 66 | 66 | 66 | 99 | 66 | 99 | 66 | 88 | 66 | 99 | 200 | 9 | 66 | 99 | 66 | 200 | 66 | 66 | 99 | 66 | 66 | 99 | 66 | 66 | 99 | 66 | 9 | 66 | 200 | 99 | 66 | 99 | 66 | 99 | 66 | 99 | 66 | 96 | 66 | 6 | 99 | 66 | 200 | 99 | 9 | 99 | 99 | 200 | 66 | 66 |
| gg | F 65 | # G | P. H. | PR: | م م م | . a. | P.R. | ۲ . ۳ . | PR | ж д ж | . H. | 2 2 | 7 0 7 0 | 86 | 주 전 0 0 | 7.2 | PR I | × 2 | PR R | PR oo | E E | PR | <u>د</u> و | r a | PR | 2 d 0 d | 2 24 | 86.0 | . E | PR | X Z | P. H. | P.R. | . Z | PR o | P. 8 | P.R. | ad. | e a | . A. | P.R. | Z 0. | H. | E E | ¥ 4 | . a. | æ 6 | 7. Y. | P.R. | P.R. | P.B. | ∡ |

418

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479 ccaaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgagt 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 geattettatecaegttteteaggeategettggagaatgtaaaaacaagaagggaggt 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 ctgttactgccaacggaaatgctggagcagctgltgtcaaggctgacacaaagccaaagg 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 ggaatgetgecaaggetgtagetaaaeccaaaggetaageetgeagaagtgaagecagetg 482
                                                                                                                                                                                                                                                                                                  244 agaacatccctcagcttttctgtgatttggtattcgacaaggagttt-agctttctcaca 302
                                 acagecttgtecacattteteaggetteaett---gaetgeacagtgaaatetggagaat
                                                                                                                                                                                      184 tigigocitiacaigtaaaggitigggaaccagaactiggitcigggaactetategacig
                                                                                                                                                                                                                                                                                                                                                                                                                                                             acttcactagttcggatgatgaggatgttcctgaagctgttcctgctcctgcccctactg
                                                                                                                                       ctgtggttttgagtgtgactgttggtggggctaaacttgttattggaacactttcacaag
                                                                                                                                                                                                                                              acaagttccctcagattagctttgatttggtttttgataaagagtttgagctttcacaca
                                                                                                                                                                                                                                                                                                                                                       geggtaccaaagcaaatgtteattteattggetacaaateeeccaacategagcaggatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC35217 standard; DNA; 1002 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0123180
990S-0123548
990S-0125788.
990S-0126264.
990S-0126785.
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99US-0130449.
99US-0130810.
99US-0130891.
99US-0131449.
99US-0132407.
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-0128714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 ctgatgatgaagatgaag 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000EP-0301439
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
08-APR-1999;
16-APR-1999;
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05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2000,
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                                 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0159293.
990S-0159294.
990S-0159295.
990S-0159329.
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990s-0161406.
990s-0161359.
990s-0161360.
990s-0161361.
990s-0161920.
                                                                             990S - 0149722.
990S - 0149723.
990S - 0149929.
990S - 0149902.
990S - 0150866.
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990S-0153758.
990S-0154018.
990S-0154039.
990S-0155139.
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990S-0156458.
990S-0156596.
990S-0157117.
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990S-0159637.
990S-0159638.
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99US-0160767.
99US-0160768.
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990S-0160981.
990S-0160989.
99US-0149368.
99US-0149175.
99US-0149426.
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99US-0151438.
99US-0151930.
99US-0152363.
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99US-0160814.
99US-0160815.
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99US-0151080.
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99US-0158369
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99US-0162142
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Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 - SEP - 1999

04 - CCT - 1999

05 - CCT - 1999

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23-APR-1999; 23-APR-1999;

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     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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| Quer Best Matc | Query Match Best Local Sir Matches 434; | Query Match 30.3%; Score 369.4; DB 21; Length 468; Best Local Similarity 95.0%; Pred. No. 5.4e-74; Matches 434; Conservative 1; Mismatches 17; Indels 5; Gaps | |
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| ٥y | 321 tr | tttcattggctacaaatcccccaacatcgagcaggatgacttcactagttcggatgatga | 380 |
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| οp | 136 to | | 195 |
| oy | 501 to | tgcagaagaggcctgaatcagacgaggaagatgagtctgatgatgaagatgaagtctg | 260 |
| qq | 196 to | | 254 |
| Qy | 561 a | aagaggatgatgactcttgagaaaggaatggatggttgatgaagatgactcagatgatga | 620 |
| qq | 255 a | | 312 |
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| QQ | 313 C | | 371 |
| ογ | 680 to | tcaacaagaagaggccaaatgaatctgtatccaaaaacaccgtctctggaaagaaggcaa 7 | 739 |
| qq | 372 to | | 431 |

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The present sequence encodes an Arabidopsis thaliana histone deacetylase designated AtHDA2B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification deacribes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase Claim 9; Fig 2B; 91pp; English. WPI; 2001-258457/27 P-PSDB; AAB67814

Sequence 1212 BP; 393 A; 238 C; 293 G; 288 T; 0 other;

altering the development of an organism.

9 540 61 atggagttctggggagttgcggtgacaccaaaaaacgctactaaggtgactcctgaagaa 120 180 420 420 480 421 gttactgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaaggcc 480 540 597 Gaps 1 gictitegeitetaaaaaaaaaaaectaacaaecteteteteteteteetegiteaaeaaaa 60 181 aaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgagtct ggtaccaaagcaaatgttcatttcattggctacaaatcccccaacatcgagcaggatgac 361 ttcactagttcggatgatgatgttcctgaagctgttcctgctcctgcccctactgct 421 gttactgccaacggaaatgctggagcagctgttgtcaaggctgacacaaagccaaaggcc aaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgagtct gatgatgaagatg-agtctgaagaaggatgatgactc-tgagaaaggaatggat-gttgat DB 22; Length 1212; .. 6 2; Indels Pred. No. 8e-248; 0; Mismatches 93.6%; Score 1139.8; 99.2%; Pred. No. 8e-2 Best Local Similarity
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1019 1073 1013 668 893 953 cgtctctggaaagaaggcaaaaccagcagcagcaccagcttctactcctcagaagacaga 779 833 774 agagaagaagaaggaggacacacccccacccccagctaagaaggtggaaagtc gaagatgactcagatgatgacgaggagg-aggattctgaggatgaagaagaggagac agagaagaagaaagaagacacaccgccacaccacacccagctaagaaggtggaaagtc teetgtgaatgetaaccagageeceaagtetggaggteaateateeggtggtaacaacaa caagaagccattcaactcaggcaaacaatttggtggttccaacaacaagggttctaacaa caagaagccattcaactcaggcaaacaatttggtggttccaacaacaagggttctaacaa gggcaagggaaaagggtagagcttaaggacgtggatcaaggaagaggttttgggttttcgag cttgttatcggatgagctattttgagtatttgcaatttctacttlcctatgtaattcagt cgtctctggaaagaaggcaaaaccagcagcagcaccagcttctactcctcagaagac--tettaagaageetgageeaateaacaagaagaggeeaatgaatetgtateeaaaaeaee tectgtgaatgetaaceagageeecaagtetggaggteaateateeggtggtaaeaaa Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss Arabidopsis thaliana DNA fragment SEQ ID NO: 30546 AAC41072 standard; DNA; 1147 BP 1200 ааааааааааддссдс 1218 1194 aaaaaaaaaagggcggccgc 1212 990S-0121825. 990S-0123180. 990S-0125788. 990S-0126748. 990S-0127462. 2000EP-0301439 (first entry) Arabidopsis thaliana 25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; EP1033405-A2 25-FEB-2000; 17-0CT-2000 06-SEP-2000 ~ 096 1020 006 1080 717 840 598 099 657 720 894 780 AAC41072 RESULT qq 염 õ 合 a q g q ŏ a ò 셤 δ g ò ð ò ò δ

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Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Scology Bidg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
         422 bp mRNA linear EST 19-MAR-2001
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White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduyd,O., Jaworskl.J.G., Ohlrogge,J. and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                                                                                                                                   224 Blochemistry, Michigan State University, East Lansing, MI 48824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Arabidopsis developing seed"
/tissue_type-"seed"
/dev_stage-"seed"
/lab_host-"B.coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone-"M44A9"
                                                                                            BE523968.1 GI:9781946
                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                      Contact: Benning, C
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Matches 413; Conservative
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1 (bases 1 to 42).
Asamizu, E., Makamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                               EST 06-SEP-2000
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu(ekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                             421 bp mRNA linear EST 06-SEP-200
CDNA clone RZ194a06F 3', mRNA sequence.
AV542939
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/tissue_type="roots"
                                                                                            Length 421;
                                                                     375 tgatgaggatgttcctgaagctgttcctgctcctgcccctactgctgttactgc
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Pred. No. 3.6e-48;
0; Mismatches 1;
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/db_xref="taxon:3702"
/clone="RZ194a06F"
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99.8%;
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Best Local Similarity 99.8%
Matches 412, Conservative
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1 (bases 1 to 504)

2 (bases 1 to 504)

3 (bases 1 to 504)

4 (bases 1 to 504)

5 (bases 1 to 504)

7 (bases 1 to 504)

8 (bases 1 to 504)

8 (bases 1 to 504)

9 (bases 1 to 504)
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/clone_lb="Lambda-PRL2"
/clone_wetcor: lambda 2ip Lox; Site_l: Sal; Site_2: Not;
Lambda PRL2 ls a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda 2ip Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.
                                                                                                                                                                                           T45874 11near EST 09-JAN-1998 9137 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133F15T7, mRNA
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                                          On Apr 14, 1993 this sequence version replaced g1:638462 Contact: Thomas Newman
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Pred. No. 6.4e-48;
0; Mismatches 16; Indels 3;
                                                                   61 AGTATATGAATATTTGCTGAAATGAGAAAGAAGACTCGAATTGCAAACACACAAA 9
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="133F1577"
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Seg primer: T7 dye primer.
Location/Qualifiers
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Best Local Similarity 95.9%;
Matches 439; Conservative 0
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 444)
Newman,T., deBrullin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,E., Ohlrogqe,J., Ralkhel,N., Somerville,S., Thomashow,M., Reizel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA597939 444 bp mRNA linear EST 19-SEP-1997
29188 Lambda-PRL2 Arabidopsis thallana cDNA clone 248C11T7, mRNA
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/clone_lib-liambda-PRL2*
/clone_lib-liambda-PRL2*
/clone_lib-liambda Zip-Lox; Site_l: Sal; Site_2: Not;
/clone_vVector: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
/clone_lib-liambda library derived from equal
quantLitles of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
gycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but acrial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The CDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed CDNA.
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Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., K.
                                                                                                                                                                        362 teactagtteggatgatgatgatgtteetgaagetgtteetgeteetgeeetaetgetg
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/strain-"var columbia"
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/clone-"248C1117"
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Email: 22313tcn@lbm.cl.msu.edu
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Spermatophyta: Magnollophyta: eudicotyledons: core eudicots:
Rosidae: eurosida II; Brassicales: Brassicaceae: Arabidopsis.
1 (bases 1 to 422)
Asamizu.E., Nakamura'r., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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CDNA clone R2106a10F 3', mRNA sequence.
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/clone_lib-"Arabidopsis thaliana roots Columbia"
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Pred. No. 1.5e-47;
0; Mismatches 17; Indels
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           Query Match 33.4%;
Best Local Similarity 95.9%;
Matches 424; Conservative
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Sperimatophyta; Magnollophyta; eudicoty; demarophyta; Magnollophyta; eudicoty;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 407)
Asamiau, E., Nakamura, Y., Sato, S. and Tabata, S.
Alarge scale analysis of cDNA in Arabidopsis thaliana; Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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/db_xref="taxon:3702"
/clone="RZ160c03F"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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| | | Description | Amino acid sequenc | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | Amino acid sequenc | Arabidopsis thalia | Arabidopsis thalia | Maize histone deac | Maize histone deac | Maize histone deac | Maize histone deac |
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| | SUMMARIES | Q 1 | AAB67814 | AAG26185 | AAG17704 | AAG38221 | AAB67813 | AAG31484 | AAG10894 | AAY28804 | AAY28803 | AAY28802 | AAY28805 |
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| , | | Query Match Length DB ID | 305 | 305 | 155 | 245 | 245 | 257 | 248 | 311 | 302 | 305 | 285 |
| | خد | Query Match | 100.0 | 0.86 | 46.6 | 37.4 | 37.4 | 37.4 | 37.1 | 34.2 | 33.7 | 33.2 | 27.4 |
| | | Score | 1589 | 1558 | 740 | 594 | 594 | 594 | 589.5 | 544 | 535 | 528 | 436 |
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| | | ABB62190 AAG54925 | | | | | | | | • | | | | | | | ABB61000 | | | | | AAY58500 | | AAG51795 | AAG51794 | AAG51793 | AAM39867 | • | AAB18 | AAG42569 |
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| 149 | 203 | 349 194 | 86 | 181 | 126 | 707 | 707 | 707 | 570 | 654 | 689 | 147 | 536 | 857 | 723 | 723 | 723 | 682 | 724 | 778 | 1162 | 1162 | 1162 | 670 | 688 | 722 | 517 | 520 | 882 | 718 |
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| 393.5 | 262.5 | 227 223.5 | 219 | 216.5 | 212.5 | 205 | 205 | 7 | 8. | 94 | 94 | 193.5 | 9 | 189 | 188 | 188 | 188 | 184.5 | 184.5 | 184.5 | 180 | 180 | m | | | | 178.5 | | | |
| 13.5 | 15 | 16 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 38 | 40 | 41 | 42 | 43 | 44 | 4.5 |

ALIGNMENTS

Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase Histone deacetylase; AtHDA2B; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation. Amino acid sequence of a histone deacetylase designated AtHDA2B. (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA. AAB67814 standard; Protein; 305 AA. Ÿ 3 24-AUG-2000; 2000CA-2316036. 99US-0383971. Tian L, (first entry) Arabidopsis thaliana. WPI; 2001-258457/27. Miki B, Brown D, N-PSDB; AAF80353. 27-AUG-1999; CA2316036-A1. 29-JUN-2001 27-FEB-2001 AAB67814; AAB67814

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                         The present sequence represents Arabidopsis thaliana histone deacetylase designated AtHDASB. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating qene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                              DDSDDDEEEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTEK 240
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         Claim 10; Fig 2B; 91pp; English.
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120
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thallana

EP1033405-A2

06-SEP-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                             Histone deacetylase; AtHDA2A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEFWGVAVTPKNATKVTPEEDSLVHISQASL-DCTVKSGESVVLSVTVGGAKLVIGTLSQ 59
                                                                                                                                                                                                                                                                             Amino acid sequence of a histone deacetylase designated AtHDA2A.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSN 297
      Arabidopsis thaliana protein fragment SEQ ID NO: 37817.
                                                 AAG31484 standard; Protein; 257 AA
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| 6 JUN-1999 8 JUN-1999 | 23 - JUN-1999; 24 - JUN-1999; 28 - JUN-1999; 28 - JUN-1999; 29 - JUN-1999; 30 - JUN-1999; 30 - JUN-1999; 30 - JUN-1999; 30 - JUN-1999; 31 - JUN-1999; 31 - JUN-1999; 31 - JUN-1999; 31 - JUN-1999; 32 - JUN-1999; 32 - JUN-1999; 33 - JUN-1999; | 3 - JUL - 1999 3 - JUL - 1999 7 - JUL - 1999 7 - JUL - 1999 8 - JUL - 1999 8 - JUL - 1999 8 - JUL - 1999 8 - ANG - 1999 5 - ANG - 1999 6 - ANG - 1999 9 - ANG - 1999 9 - ANG - 1999 1 - ANG - 1999 |
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| | e 594; DB 21; Length 257; I. No. 1.1e-39; Ilsmatches 63; Indels 58; Gaps AASL-DCTVKSGESVVI,SVTVGGAKI,VIGTLSQ 59 [14]: |
|--|--|
| 99085-0149108. 99085-0149108. 99085-014912. 99085-0149722. 99085-0149923. 99085-0149902. 99085-0150864. 99085-0151080. | 990S-0161992. 990S-0161993. 990S-0162193. 11ty 50.7%; Pred nservative 26; M PKNATKYPEEDSLVHISG |
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                    : ||: ||||||||||||| | :|:|||||||| : | ::|: | |||| enipqlfcdlvfdkefelshtwgkgsvyfvgyktpniepqgy-seeeeeeeeevpa---- 115
                                                      EDDSDDDEEEDSEDEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTE 239
                                                                            240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSN 297
                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 9401.
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                                                                                                                           AAG10894 standard; Protein; 248
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99US-0125788.
99US-0126745.
99US-0126764.
99US-01267834.
99US-0128714.
99US-0138714.
99US-0130077.
99US-0130891.
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23-MAR-1999;

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19-APR-1999;

11-APR-1999;

23-APR-1999;

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06-MAY-1999;

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06-MAY-1999;

06-MAY-1999;

11-MAY-1999;

11-MAY-1999;

14-MAY-1999;

21-MAY-1999;

21-MAY-1999;
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MAY-1999;
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PR 01-JUN-1999; 99US-0137528.
PR 03-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137528.
PR 10-JUN-1999; 99US-0137734.
PR 10-JUN-1999; 99US-013864.
PR 10-JUN-1999; 99US-0139454.
PR 10-JUN-1999; 99US-0139452.
PR 10-JUN-1999; 99US-0139452.
PR 10-JUN-1999; 99US-0139452.
PR 10-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139451.
PR 22-JUN-1999; 99US-0139451.
PR 23-JUN-1999; 99US-0139451.
PR 23-JUN-1999; 99US-0140333.
PR 23-JUN-1999; 99US-0140333.
PR 23-JUN-1999; 99US-0144333.
PR 23-JUN-1999; 99US-0144333.
PR 13-JUL-1999; 99US-0144333.
PR 13-JUL-1999; 99US-0144333.
PR 13-JUL-1999; 99US-0144333.
PR 13-JUL-1999; 99US-0144333.
PR 22-JUL-1999; 99US-0144333.
PR 23-JUL-1999; 99US-014508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is maize histone deacetylase encoded by HD cDNA belonging to family 2, ZmHD2. This enzyme responsible for removing acetyl modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind requiatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transpenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New deacctylase genes, used for producing transgenic plants which have increased disease resistance
                                                                                                                                             180 EDDSDDDEEEDSEDEREETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPOKTE 239
                                                                                                                              DKFPQ1SFDLVFDKEFELSHSGTKANVHF1GYKSPN1EQDDFTSSDDEDVPEAVPAPAT 119
                                                                                                                                                                                           120 AVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVD 179
                                                                                                                                                                                                                                                                                       153 eddsdg---eds--eeeeptpkkpas-skkranettpkapvsakkakvav----tpqktd 202
                                  Caps
                                                               1 MEFWGVAVTPKNATKVTPEEDSLVHISQASI, DCTVKSGESVVI,SVTVGGAKLVIGTI,SQ 59
                                                                                 240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSN 297
                                                                                                                                                                                                                                                                                                                                       203 ek-------kkggka---anxspksasqvscg-scktfnsgnal-eshnkakh 244
37.1%; Score 589.5; DB 21; Length 248; 49.7%; Pred. No. 2.3e-39; Live 27; Mismatches 68; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 79-80; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY28804 standard; protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crane VC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize histone deacetylase-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0080563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                 Conservative
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                Similarity
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                                 Matches 148;
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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                         Maize histone deacetylase; HD; HD cDNA; family 2, ZmHD2; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New deacetylase genes, used for producing transgenic plants which have increased disease resistance
                                                                                                               KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTA 120
                                                                                                                                                                                                                           KAKPAAAPASTPQKTEKKKGG-HTATPHPAKKGGKSPVN----ANQSPKSGGQSSGGNNN 278
                                       Gaps
                                                            9
                                                                              1 mefwglevkpgstvkcepghgfilhvsqaalgeskks-dsalmyvkvddkklaigtlsid 59
                                                          MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD
                                                                                                                                          121 VTANGNAGAAVVKADTKPKAKPAE-------VKPAEEKPESDEEDESDDEDES
                                                                                                                                                                                  167 EEDDDSE-KGMDVDEDDSDDDEEEDSEDEEEE--TPKKPEPINKKRPNESVSKTPVSGK
                                       42;
                    Length 311;
                  34.2%; Score 544; DB 20; Length 31
43.2%; Pred. No. 1.3e-35;
ive 37; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 76-77; 87pp; English.
                                                                                                                                                                                                                                                                                                                                          AAY28803 standard; protein; 302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                   279 KKPFNS--GKQFGGSNNKGSNK 298
                                                                                                                                                                                                                                                                                       283 sktfnsemalgahskanmgpne 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0080563
                                                                                                                                                                                                                                                                                                                                                                                                      Maize histone deacetylase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US07370
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease response promoter,
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                     139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Briggs SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-611038/52.
                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baldwin DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-0CT-1999
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                   Query Match
                              Best Local
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                                      Matches
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producing transgenic plants with increased disease resistance.
Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New deacetylase genes, used for producing transgenic plants which have increased disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEED--DDSEKGMDV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEDDSDDDEEEDSEDEEEEE--TPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYK$PNIEQDDFTSSDDEDVPEAVPAPAPTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is maize histone deacetylase encoded by HD cDNA
                                                                                                                                                                                                                                                                                                 22; Gaps
                                                                                                                                                                                                                                                                                                                                                       1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60
                                                                                                                                                                                                                                                                                                                                                                                                             1 mefwglevkpgstvkcepgygfvlhlsgaalgeskks-dnalmyvkiddgklaigtlsvd
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 KTEKKKGG--HTATPHPAKKGGKSPVNANQS------PKSGG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93:
                                                                                                                                                                                                                                    33.7%; Score 535; DB 20; 43.8%; Pred. No. 6.6e-35;
                                                                                                                                                                                                                                                                                              44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crane VC
                                                                                          regulated by histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28802 standard; protein; 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease response promoter.
                                                                                                                                                                                                                                                                Best Local Similarity 43.8%
Matches 124; Conservative
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                                                                                                                                                      Sequence
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other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New deacetylase genes, used for producing transgenic plants which have
                                                                                                                                                                                                                               DEDDSDDDEEEDSEDEEEE--TPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQ 236
                                                                                                                                                                                                                                                                                                                             KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTA 120
                                                                                                                                                                                                                                                                 121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEED--DDSEKGMDV 178
                                                                                                                                                                   1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60
                                                                                                                                                                                            mefwglevkpgstvkcepgygfvlhlsqaalgeskks-dnalmyvkiddqklaigtlsvd 59
                                                                                                                                              22;
                                                                                                                     Length 305;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                           KTEKKKGG--HTATPHPAKKGGKSPVNANQS-----PKSG 269
                                                                                                                                               93;
                                                                                                                      DB 20;
                                                                                                                      Score 528; DB 20;
Pred. No. 2.4e-34;
                                                                                                                                             44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY28805 standard; protein; 285
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                                                                                                                    33.2%;
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                                                                                                                                             Conservative
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                                                                                                                                   Similarity
                                                                                   305 AA;
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                                                                                                                                             Matches 123;
                                                                                   Sequence
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Best Local
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The present sequence is maize histone deacetylase encoded by HD cDNA

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
belonging to family 2, ZmHD2. This enzyme responsible for removing acety modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKS--PNIEQDDFTSSDDEDV-PEAVPAPA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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; Pred. No. 5e-27;
49; Mismatches 110;
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990S-0128234.
990S-0128714.
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99US-0123548.
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36.0%;
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Matches 114; Conservative
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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08-APR-1999;
16-APR-1999;
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99US-0144325
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99US-0144333
 16-APR-1999;
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30-APR-1999;
04-MAY-1999;
06-MAY-1999;
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9908-0160741.
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9908-0160768.
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990S-0128234.
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PR 22-701.1999 9918-0146634

PR 22-701.1999 9918-0146694

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PR 22-701.1999 9918-0146206

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PR 23-701.1999 9918-0146226

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PR 23-701.1999 9918-014626

PR 23-701.1999 9918-014629

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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.7%; Score 345.5; DB 21; Length 208; Best Local Similarity 39.6%; Pred. No. 5.8e-20; Matches 93; Conservative 27; Mismatches 66; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                         1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGES------VVLSVTVGGAKLV 53
                                                                                                                                                                                                                                                                                                                                    Immunophilin; moth; insect cell; nuclear; immunosuppression; drug; transplant; tissue graft.
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/note- "AP motif"
215..218
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148..149
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135..138
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111..114
/note= "EEAP motif"
124
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990S-0159584
990S-0160741
990S-0160768
990S-0160770
990S-0160815
990S-0160815
990S-0160980
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990S-0161406
990S-0161360
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                      99US-0159331
99US-0159637
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14 OCT - 1999)
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Domain
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AAW68010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 liqvpldlyfksgdsvsfltngkcnvhltgyldpefeedledeeeaeeeeeeeeapplvp 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 T---AVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEED------ESDDED 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 68; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
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/note= "EEAP motif"
219..223
/note= "putative nuclear localisation signal"
                                                                                                                     /note- *putative nuclear localisation signal * 272..275 /note- *putative nuclear localisation signal * note- *putative nuclear localisation signal * 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 100 / 1
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19.6%; Score 311; DB 20; Length 412;
Bost Local Similarity 31.0%; Pred. No. 7.3e-17;
Matches 100; Conservative 39; Mismatches 116; Indels 66
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96US-0741134.
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298..302
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                    Arabidopsis thaliana protein fragment SEQ 1D NO: 6998.
                AAG09171 standard; Protein; 203 AA.
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99US-0132485.
99US-0132486.
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99US-0138847.
99US-0139119.
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                                                  17-OCT-2000 (first entry)
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14 - JUN - 1999;
16 - JUN - 1999;
16 - JUN - 1999;
17 - JUN - 1999;
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25-MAR-1999;
29-MAR-1999;
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GenCore version 4.5
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Run on:

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SUMMARIES

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| 1 | 544 | 34.2 | 311 | 7 | US-09-282-305-16 | Sequence 16, Appl | |
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| 12 | 180 | 11.3 | 1162 | ~ | US-08-728-323A-2 | 2, | |
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| 24 | 164 | 10.3 | 542 | _ | | 7 | |
| 25 | 164 | 10.3 | 542 | ٣ | US-09-032-365A-13 | 13, | |
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| 27 | 161.5 | 10.2 | 905 | 7 | US-09-357-014-9 | 6 | |

| Sequence 7, Appli Sequence 7, Appli | Sequence 28, Appl | Sequence 28, Appl | 28, | Sequence 28, Appl | Sequence 28, Appl | Sequence 26, Appl | 26, | 26, | 194 | | Sequence 190, App | | • | Sequence 20, Appl | | 68, |
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| 161.5 161.5 | 156 | 156 | 155.5 | 155.5 | 155.5 | 155.5 | 155,5 | 155,5 | 149 | 149 | 149 | 149 | 149 | 149 | 148.5 | 146 |
| 28 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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| 279 | SGUT 10-282-305-16 Sequence 16, Application US/09282305 Sequence 16, Application US/09282305 Sequence 16, Application US/09282305 Sequence 16, Application US/09282305 APPLICANT: Baldwin, Donald A. APPLICANT: Eniggs, Steven P. APPLICANT: Eniggs, Steven P. APPLICANT: Eniggs, Steven P. TILLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REPERBNCE: 57194-44, CURRENT APPLICATION NUMBER: US/09/282,305 FRIOR APPLICANT: 1999-04-03 PRIOR APPLICANT: 1999-04-03 PRIOR PALE OF TILLE OF THE US OF THE | THE WINDS AND THE PROPERTY OF |
| 279 KKPFNSGKOFGGSNNKGSNK 298 | SGUT 10-282-305-16 Sequence 16 Application US/09282305 Sequence 16 Application US/09282305 Sequence 16 Application US/09282305 Sequence 16 Application US/09282305 Sequence 16 Application: APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Daniel A. APPLICANT: CIARCHIT Baldwin, Donald A. APPLICANT: CIARCHIT Baldwin, Daniel C. TITLE OF INTENDITION: Maize Histone Deacetylases And Their Uses FILE REPERBNCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: US/09.83 PRIOR PLING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOCTWARE: PRIOR PLING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOCTWARE: SOCTWA | 229 KAKVATDDAOKTGGKGATHVATDHAKGKTDANNKSTERSDKSGG-SVDCKSC |
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| | SIGUT 1 | 224 KAKPAAAPASTPQKTEKKKGG-HTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNN |
| 224 KAKPAAAPASTPQKTEKKKGG-HTATPHPAKKGGKSPVNANQSPKSGGOSSGGNNN | SIGUT 1. 199-282-305-16 199-282-305-16 289-282-305-16 289-282-305-16 289-281-305-305-305 APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Maize Histone Deacetylases And Their Uses FILE OF INVENTION: Maize Histone Deacetylases And Their Uses CURRENT PLING DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1998-04-03 ROUBEN APPLICATION NUMBER: US/08/282,305 CURRENT PAPEL DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 3.7; Mismatches 104; Indels 42; Ga CORGANISM: 2ea mays 109-282-305-16 1 MEFWGLEVKPGSTYKCEPGHGFILHVSQASIDCTVKSGESVUSYTVGGAKLVIGTILSID 1 MEFWGLEVKPGSTYKCEPGHGFILHVSQASIDCTVKSGESVUSVTVGGAKLVIGTILSID 61 KFPQISFDLYPDKREFELSHSGTKANHFIGYKSPNISODEFESEDESDDEDEE 1 | |
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| | 109-282-305-16 69quence 16, Application US/09282305 3EMERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: MALZE HIStone Deacetylases And Their Uses APPLICANT: Crane, Virginia C. TITLE OF INVENTION: MALZE HIStone Deacetylases And Their Uses TITLE OF INVENTION: MALZE HISTONE DATE: 1999-03-31 PRIOR FILING DATE: 1999-04-3 PRIOR PILING DATE: 1999-04-3 PRIOR PILING DATE: 1999-04-3 PRIOR PILING DATE: 1999-04-3 NUMBER OF SEQ ID NOS: 18 SECTIONE: PATORICATION NUMBER: 60/080,563 PRIOR PILING DATE: 1999-04-3 NUMBER OF SEQ ID NOS: 18 SECTIONE: PATORICATION NUMBER: 60/080,563 PRIOR PILING DATE: 1999-04-3 NUMBER OF SEQ ID NOS: 18 SECTIONE: PATORICATION NUMBER: 60/080,563 PRIOR PILING DATE: 1999-04-3 SECTIONE: 11 | 167 EEDDDSE-KGMDVDEDDSDDDEEEDSEDEEEETPKKPEPINKKRPNESVSKTPVSGK |
| 167 EEDODSE-KGMDVDEDDSDDDEEDSEEEETPKKPEPINKKRPNESVSKTPVSGK 11 | 109-282-305-16 109-282-305-16 29atent No. 628/843 25BERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crand Maize Histone Deacetylases And Their Uses TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses TYPE: PRT OF MAICH TOWN UNDER: US/09/282,305 DRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOCTHARE: Patentin Ver. 2.0 SOCTHARE: Patentin Ver. 2.0 LENGTH: 311 TYPE: PRT ORGANISM: Zea mays O9-282-305-16 LENGTH: 311 MEFWGLAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSYTVGGAKLVIGTLSQD IIIII: | |
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| Ob-282-305-16 Duery Match 34.2%; Score 544; DB 4; Length 311; Best Local Similarity 43.2%; Pred. No. 6.8e-39; Matches 139; Conservative 37; Mismatches 104; Indels 42; Gaaltches 139; Conservative 37; Mismatches 104; Indels 42; Gallatches 139; Conservative 37; Mismatches 104; Indels 42; Gallatches 139; Conservative 37; Mismatches 104; Indels 42; Gallatches 11111; I I I I I I I I I I I I I I I I | 18.2 105-16 ence 16, Application US/09282305 nt No. 6287843 RAL INFORMATION LICANT: Briggs, Steven P. LICANT: Crane, Virginia C. LICANT: Crane, Virginia C. LE OF INVENTION: Maize Histone Deacetylases And Their E REFERENCE: 5718-44, RENT APPLICATION NUMBER: US/09/282,305 RR PRILING DATE: 1999-03-31 OR RILING DATE: 1999-04-03 OR FILING DATE: 1998-04-03 ENER OF SEQ ID NOS: 18 TWARE: Patentin Ver. 2.0 ID NO 16 NGTH: 311 | ; ORGANISM: Zea mays |
| ORGANISM: Zea mays -09-282-305-16 Ja.28; Score 544; DB 4; Length 311; Best Local Similarity 43.28; Pred. No. 6.88-39; Matches 139; Conservative 37; Mismatches 104; Indels 42; Ga atches 139; Conservative 37; Mismatches 104; Indels 42; Ga illil: | 12-305-16 ence 16, Application US/09282305 nt No. 6287643 RIAL INFORMATION: LICANT: Ballowin, Donald A. LICANT: Briggs, Steven P. LICANT: Crane, Virginia C. LECONTION MUMBER: US/09/282,305 RENT FILING DATE: 1999-03-31 OR APPLICATION NUMBER: 05/080,563 OR PELING DATE: 1999-04-03 BER OF SOI ID NOS: 18 TWARE: PATENTIN VET: 2.0 ID NO 16 | ; TYPE: PRI |
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| PRIOR PILLING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILLING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 188 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 16 LENGTH: 311 TYPE: PRT O9-282-305-16 O9-282-305-16 Adatches 139; Conservative 37; Mismatches 104; Indels 42; Ga datches 139; Conservative 37; Mismatches 104: Indels 42; Ga datches 139; Conservative 37; Mismatches 104: Indels 42; Ga datches 139; Conservative 37; Mismatches 104: Indels 42; Ga datches 139; Conservative 37; Mismatches 104: Indels 42; Ga datches 139; Conservative 37; Mismatches 104: Indels 42; Ga left 1111: | 1 282-305-16 ence 16, Application US/09282305 nt No. 6287843 RAL INFORMATION: LICANT: Baldwin, Donald A. LICANT: Brigas, Steven P. LICANT: Crane, Virginia C. LECANT: Crane, Virginia C. LE REFERRALE: 5718-44. | CHREENT ADDITIONATIONED INCOME. 305 |
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| TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/090.563 PRIOR APPLICATION NUMBER: 05/080,563 PRIOR FILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 16 LENGTH: 311 TYPE: PRT ORGANISM: Zea mays 09-282-305-16 34.2%; Score 544; DB 4; Length 311; ORGANISM: Zea mays 09-282-305-16 10-282-305- | 1 282-305-1 ence 16, nt No. 62 RAL INFOF LICANT: LICANT: | ; APPLICANT: Crane, Virginia C. |
| APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44. CURRENT APPLICATION NUMBER: US/09/282,305 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 311 TYPE: PRY ORANISH: Zea mays 09-282-305-16 LENGTH: 311 MEFWGVAVPENDIALLY 43.2%; SCOTE 544; DB 4; Length 311; Best Local Similarity 43.2%; Pred. No. 6.8e-39; MACCAN SEC. 100: 100: 100: 100: 100: 100: 100: 100 | 1 282-305-1 ence 16, nt No. 62 RAL INFOR | Briggs, Steven F |
| APPLICANT: CIAGE, SUCHER FOR THE FORESTANT: CIAGE, SUCHERINE CIAGE, VIGIDIA C. TITLE OF INVENTION: Maice Histone Deacetylases And Their Uses FILE REFERENCE: 578-4. FILE REFERENCE: 578-4. CURRENT APPLICATION NUMBER: 08/09/282,305 CURRENT PILING DATE: 1998-03-31 PRIOR PAPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PATON NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 34.24; Score 544; DB 4; Length 311; Best LOCAL Similarity 43.24; Pred. No. 6.88-39; NUMBER OF SEQ INTROPURE SECRETARY NUMBER: PATON NUMBER SEGGENOR INTROPURS SEGGENOR INTROPURS SEGGENOR INTROPURS SEGGES SUPERS S | 1 282-305-1 ence 16, nt No. 62 RAL INFOF | 1 4011045 |
| APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maice Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44 FILE REPERBENE: 5718-44 FILE REPERBENE: 5718-45 FRIOR PAPLICATION NUMBER: 05/09/282,305 CURRENT APPLICATION NUMBER: 60/080,563 PRIOR PAPLICATION NUMBER: 60/080,563 PRIOR PAPLICATION NUMBER: 60/080,563 NUMBER OF SEQ ID NOS: 18 SOOFWARE: Patentin Ver. 2.0 SED ID NO 16 LENGTH: 311 TYPE: PRT ORGANISH: Zea mays 09-282-305-16 MERWGVAPPRINTYPEEDSLUHSOASIDCTVKSGESVULSVTVGGAKLVIGTLSOD 1111: 11 1 1 1 1 1 1 1 1 | 1 282-305-1 ence 16, nt No. 63 RAL INFOF | Donald |
| APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. APPLICANT: Crane, Virginia C. APPLICANT: Crane, Virginia C. CTATE, Briggs, Steven P. APPLICANT: Crane, Virginia C. CURRENT Briggs, Steven P. FILE REFERENCE: 5718-44. CURRENT APPLICATION NUMBER: 08/09/282,305 FRIOR APPLICATION NUMBER: 06/080,563 FRIOR APPLICANTON NUMBER: 06/080,563 FRIOR NUMBER OF SECULT OF S | 1 282-305-1 ence 16, nt No. 62 | |
| APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Eriggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INTWININA Haize Histone Deacetylases And Their Uses FILE REPERNET: 5718-44. TITLE OF INTWINION: Haize Histone Deacetylases And Their Uses FILE PRETERNET: 5718-44. CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-04-03 PRIOR PAPLICATION NUMBER: 06/080,563 PRIOR PAPLICATION NUMBER: 66/080,563 PRIOR PAPLICATION NUMBER: 66/080,563 PRIOR PAPLICATION NUMBER: 66/080,563 PRIOR PAPLICATION NUMBER: 1999-04-03 SOFTWARE: Patentin Ver. 2.0 SOFTWARE SO | 1 282-305-1 ence 16, | Parent NO. 026/043 |
| APPLICANT: Baldwin: APPLICANT: Baldwin: APPLICANT: Baldwin: APPLICANT: Baldwin: APPLICANT: Baldwin: APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REPERENCE: 5718-44. CURRENT APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: 1999-04-03 PRIOR APPLICATION NUMBER: 06/080,563 PRIOR APPLICATION NUMBER: 06/080,000,000,000, | 1 282-305-1 ence 16 | · Datant And Applet - Constant of Constant |
| atent No. 6287843 SBREAL INFORMATION; APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE OF INVENTION NUMBER: 1999-03-31 FRIOR PPLICATION NUMBER: 1999-03-31 PRIOR PLICATION NUMBER: 60/080,563 PRIOR PLICATION NUMBER: 60/080,563 PRIOR PLICATION NUMBER: 60/080,563 PRIOR PLICATION NUMBER: 60/080,563 NUMBER: Patentin Ver. 2.0 SECTIVARE: PATENTING DATE: 1988-04-03 SECTIVARE: 1988-04-03 SECTIVAR | RESULT 1 US-09-282-305-16 | : Sequence 16. Application US/09282305 |
| Sequence 16, Application US/09282305 Settent No. 6287843 Settent No. 6287843 APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Baldwin, Donald A. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REPRENCE: 571844, CURRENT APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: US/09/282.305 PRIOR APPLICATION NUMBER: US/080.563 PRIOR PLILING DATE: 1999-04-03 NUMBER OF SEQ ID 005: 18 SOCTWARE: PART OF SEQ ID 005: 18 S | RESULT 1 | US-09-282-305-16 |
| O'9-282-305-16 O'9-282-305-16 Satent No. 6287843 SAPLICANT: Baldwin, Donald A. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE OF STIRG DATE: 1998-04-03 FRIOR PRIOR PLOATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOCTWARR: Patentin Ver. 2.0 SEQ ID NO 16 SEQ | | RESULT 1 |
| SELOT 1 SERVAR INTORNATION: APPLICANT: Baldwin, Donald A. BRIGGRANISM: Canal B. APPLICANT: Baldwin, Donald A. BRIGGRANISM: Lilly B. APPLICANT: Baldwin, Donald A. BRIGGRANISM: Loa mays APPLICANT: Baldwin, Donaldwin, Donaldw | | |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 DEDDSDDDEEEDSEDEEEEE--TPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 33.7%; Score 535; DB 4; Length 302;
Best Local Similarity 43.8%; Pred. No. 3.8e-38;
Matches 124; Conservative 44; Mismatches 93; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEFWGLEVKPGSTVKCEPGYGFVLHLSQAALGESKKS-DNALMYVKIDDQKLAIGTLSVD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60
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Sequence 12.3 Application US/09282305

Patent No. 6287843

GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Baldwin, Steven P.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
TITLE OF INVENTION WHER: US/09/282,305

CURRENT APPLICATION NUMBER: US/09/282,305

CURRENT PILING DATE: 1999-03-31

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 305
                                                                  GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Baldwin, Donald A.
APPLICANT: Baldwin, Donald A.
APPLICANT: Grane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
CURRENT FILE TOTALION NUMBER: 05/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 KTEKKKGG--HTATPHPAKKGGKSPVNANQS-----PKSGG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 KTGGKKGAAVHVATPHPAK--GKTIVNNDKSVKSPKSAPKSGG 274
US-09-282-305-14; Sequence 14, Application US/09282305; Patent No. 6287843
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: ORGANISM: Zea mays

US-09-282-305-12
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US-09-282-305-14
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LENGTH: 302
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                                                                                                                                                                                                                                              121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDEDESEED--DDSEKGMDV 178
                                                                                                                                                                                                                                                                                                                            179 DEDDSDDDEEEDSEDEEEEE--TPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQ 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 VDEDDSDDDEEEDSEDEEEETPKKPE-PINKKRPNESVSKTPVSGKKAKPAAAPASTPQ 236
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                                                                            1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crans.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
33.2%; Score 528; DB 4; Length 305; 43.6%; Pred. No. 1.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.4%; Score 436; DB 4; Length 285; 36.0%; Pred. No. 9.6e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   234 KTGGKKGAAVHVATPHPAK -- GKTIVNNDKSVKSPKSAPKSG 273
                                                                                                                                                                                                                                                                                                                                                                                                           237 KTEKKKGG--HTATPHPAKKGGKSPVNANQS-----PKSG 269
                                        44; Mismatches
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                                        Matches 123; Conservative
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                   Best Local Similarity
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LENGTH: 285
Query Match
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  APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TILE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AVPAPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOUTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,114
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.0%; Score 206; DB 2;
Lilarity 23.2%; Pred. No. 1.2e-09;
Conservative 31; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                        Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF-0451 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                           251 PAKKGGKSPVNANQSPK-SGGQS 272
                                                                                            287 PEAKKEEAPVEKKEKKQIAGGVS 309
                                                                                                                                                                                                  Sequence 3, Application US/08990114
Patent No. 5924A75
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 SEEDDDSEKGMDVDEDD-----
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 EQDDFTSSDDEDVPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 66; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LIBRARY: GenBe
; CLONE: 128842
US-08-990-114-3
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                                                                                                                                                                          US-08-990-114-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AKNKRKLENANDATANKKAKPDKKAGKNSAPAAESDSDDDDEDQLQKFLDGEDIDTDEND 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESEEDDDSEKGMDVDEDDSDDDEE----EDSEDEFEEFTPKKPEPINKKRP----- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 FPQISFDLVFDKEFELSH-SGTKANVHFIGYKSPNIEQD--DFTSSDDEDVPEAVPAPAP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ESDDED 164
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LITWACK, Gerald
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
TITLE OF INVENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
TITLE OF INVENTION: AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FWGLIMEPNKRYTQVV - - - EKPFHISQAAMDISTGDNDPCQVMVVVDGKNFLVCTLQKGK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 FWGVAVTP-KNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQDK 61
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5861498ris
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.6%; Score 311; DB 2; Length 412; Best Local Similarity 31.0%; Pred. No. 6.8e-19; Matches 100; Conservative 39; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 T---AVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: Windows 3.11
SOFTWARE: WordPerfect for Windows 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-2090
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                               Sequence 2, Application US/08741134
Patent No. 5861498
269 GSASALESHOKAKKHEA 285
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LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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                                                                                            US-08-741-134-2
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| ò | 206 INKKRPNESVSKTPVSGKKAKPAAAPAST | : : : : DD 155 DDSDEDEDEEEDFEPPVVKGKQG |
|------------|---|---|
| qa | : :: | QY 206 INKKRPNESVSKTPVSGKKAKPAAAPAS |
| δ | 240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFN 283 | Db 207 EDSEEEEAMEITPAKGKKAPAKVVPVK |
| qq | 267 EEEEEEPVKPAPGKR-KKEMTKQKEVPEAKKQKVEGSESTIPFN 309 | Qy 240 KKKGGHTATPHPAKKGGKSPVNANGSPK |
| RESULT | | DD 267 BEBBBPVKPAPGKR-KKEMTKQKEVPE |
| US-0 | US-09-241-333-3 : Secuence 3. Annlication HS/A0241233 | 0 511240 |
| G G | Patent No. 6313266 | US-07-814-964-11 |
| | .NEKAL INFORMATION: APPLICANT: Bandman, Olga | ; Sequence 11, Application US/07814964 ; Datent No. 5359047 |
| | Yue, Henr | GENERAL INFORMATION: |
| | APPLICANT: Corley, Neil C. APPLICANT: Shah, Purvi | |
| . •• | NVENTION: H | : Bruhn, Suzanne |
| | 88 | <pre>; APPLICANT: Pil, Pieter M. ; APPLICANT: Brown, Steven</pre> |
| ٠ | ADDRESSEE: Incyte Pharmaceuticals, Inc. | ; APPLICANT: Kellett, Patti |
| | | ; APPLICANT: Essigmann, John M. ; APPLICANT: Lippard, Stephen J. |
| ٠ | STATE: CA | TITLE OF INVENTION: DNA Structur |
| ٠., | ZIP: 94304 | NUMBER OF SEQUENCES: 13 |
| | COMPUTER READABLE FORM: | ; CORRESPONDENCE ADDRESS: |
| | COMPUTER: IBM Compatible | STREET: 2 Militia Drive |
| | OPERATING SYSTEM: DOS | ; CITY: Lexington |
| | LICATION DATA: | COUNTRY: USA |
| | APPLICATION NUMBER: US/09/241,333 | , ZIP: 02173 |
| | CLASSIFICATION: | ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk |
| | PRIOR APPLICATION DATA: Application nimber: 08/990.114 | COMPUTER: IBM PC Compatible |
| | FILING DATE: | SOFTWARE: Patentin Release #1 |
| ٠ | ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. | CURRENT APPLICATION DATA: |
| | 749 | FILING DATE: 19911226 |
| | REFERENCE/DOCKET NUMBER: PF-0451 US FELECOMMUNICATION INFORMATION: | CLASSIFICATION: 435 |
| | TELEPHONE: 650-855-0555 TRIFFAX: 650-845-4166 | APPLICATION NUMBER: US 07/539, |
| | IELEX: 050-045-4100 TELEX: | ; FILING DATE: 18-JUN-1990; ATTORNEY/AGENT INFORMATION: |
| H | INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: | ; NAME: Granahan, Patricia |
| | LENGTH: 714 amino acids | REFERENCE/DOCKET NUMBER: MIT-4 |
| | TYPE: amino acid STRANDEDNESS: single | ; TELECOMMUNICATION INFORMATION: |
| ••• | ear | • |
| | LIBRARY: GenBank | : INFORMATION FOR SEQ ID NO: II |
|); US-0 | CLONE: 128842 -09-241-333-3 | 7 |
| | | X |
| ð | 13.0%; Sec | ; TOPOLOGY: 11near ; MOLECULE TYPE: protein |
| W Be | • |) ORIGINAL SOURCE: |
| į | CONTRACTOR | 8 |
| à i | | ; CLONE: Drosophila SSRP (predic |
| QQ | 35 EEEDDSSGEEVVIPQKKGKKATATPAKKVVVSQTKKVAVPTPAKKAAVTPGKKAAATPAK 94 | : NAME/KEY: Domain : LOCATION: 458::507 |
| οy | 118PTAVTANCNAGAAVVKADTKPKAKPAEVKPAEEKPESDEBDESDEBDE 165 | ; OTHER INFORMATION: /label- Aci |
| qa | 95 KAVTPAKAVATPGKKGATQAKALVATPGKKGAVTPAKGAKNGKNAKKEDSDEDEDDDDE 154 | NAME/EN: Domain |
| óý | 166 SEEDDDSEKGMDVDEDDSDDDEEEDSEDSEDEEETPKKPEP 205 | ; LUCATION: 518.54/ ; OTHER INFORMATION: /label- Bas |
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KAKNVAEEDDODDEEEDEDEEDEEBEBE 266
                                                                                                                                                                                          re Specific Recognition
Uses Therefor
                                                   KSGGOSSGGNNNKKPFN 283
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EAKKQKVEGSESTTPFN 309
                                                                                                                                                                                                                        nith & Reynolds, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 EEISSVNFARSG----GSTRSFDFEVTLKNGTVHIFSSIEKEEYAKL-FDYITQKKLHV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 SHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVD---EDDSDDDE----- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 DSDGAKKKKEKKSEKKEKKEKKHKEKERTKKPSKKKKDSGKPKRATTAFMLWLNDTRESI 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SPVNANQSPKSGGQS---S 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574 KRENPGIKVT-EIAKKGGEMWKELKDKSKWEDAAAKDKQRYHDEMRNYKPEAGGDSDNEK 632
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  19 EEDSLVHISQASLDCTVKSGESVVLSVTV-GGAKLVIGTLSQDKFPQISFDLVFDKEFEL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                             Length 723;
                                                                                                                                                                                                                                                                                                                      Query Match 11.8%; Score 188; DB 1; Length 723
Best Local Similarity 23.5%; Pred. No. 4.2e-08;
Matches 76; Conservative 53; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Donablue, Brian A.
APPLICANT: Donablue, Brian A.
APPLICANT: Donablue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TILE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STARET: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                         ; NAME/KEY: Domain
; LOCATION: 657..723
; OTHER INFORMATION: /label- Mixed Charge
US-07-814-964-11
                                                                                                                                          /label= Basic II
NAME/KEY: Domain
LOCATION: 547..620
COCATION: 747..620
FOTHER INFORMATION: /label- HMG-box
FOTHER: Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-258-442-11
; Sequence 11, Application US/08258442
; Patent No. 5670621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 GGKSSKKRTEPSPSKKANTSGS 655
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MEDIUM TYPE: Floppy
                                                                                                                 LOCATION: 632..649
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02173
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                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 EEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKK--AKPAAAPAS-----TPQKT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 EKKKGGHTATPHPAKKGGK-----S 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 EEISSVNFARSG----GSTRSFDFEVTLKNGTVHIFSSIEKEEYAKL-FDYITQKKLHV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 SHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVD---EDDSDDDE----- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%; Score 188; DB 1; Length 723; 23.5%; Pred. No. 4.2e-08; tive 53; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 657..723
; OTHER INFORMATION: /label- Mixed Charge
US-08-258-442-11
APPLICATION NUMBER: US/08/258,442
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 1B-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO: 11:
INFORMATION FOR SEQ ID NO: 11:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Basic II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Domain
LOCATION: 518.547
OTHER INFORMATION: /label- Basic I
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSRP (predicted)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- HMG-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGNNNKKPFNSGKQFGGSNNKGS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 23,55,
forbes 76; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Domain
LOCATION: 458..507
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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ZIP: 02173
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                                       APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Essigmann, John M.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Brown, Steven
APPLICANT: APILICANT: Relieft, Patil
JITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Patent Administrator, Testa, Hurwitz & Thibeault
STRRET: 53 State Street
CITY: Boston
STATE: V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
INFORMATION FOR SKO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : LOCATION: 657..723
; OTHER INFORMATION: /label- Mixed Charge US-08-328-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Basic II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label- Basic I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNGANISM: Drosophila melanogaster IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- HMG
US-08-328-809-6; Sequence 6, Application US/08328809; Patent No. 5705334; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 458..507
OTHER INFORMATION:
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LOCATION: 547..620
OTHER INFORMATION:
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LOCATION: 632..649
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   188 EEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKK--AKPAAAPAS-----TPQKT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SPVNANQSPKSGGQS---S 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 SHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTK 137
Query Match 11.8%; Score 188; DB 1; Length 723;
Best Local Similarity 23.5%; Pred. No. 4.2e-08;
Matches 76; Conservative 53; Mismatches 110; Indels 84; Gaps
                                                                                                              19 EEDSLVHISQASLDCTVKSGESVVLSVTV-GGAKLVIGTLSQDKFPQISFDLVFDKEFEL, 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Donative, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Brown, Suzanne L.
APPLICANT: Brown, Steven
APPLICANT: Fislett, Patti
APPLICANT: Essienn, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentLI Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11107
FILING DATE: 19921218
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECHONE: 617.861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US92-11107-11; Sequence 11, Application PC/TUS9211107; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 GGNNNKKPFNSGKQFGGSNNKGS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 GGKSSKKRKTEPSPSKKANTSGS 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lexington
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 EEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKK--AKPAAAPAS-----TPQKT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 EEDSLVHISQASLDCTVKSGESVVLSVTV-GGAKLVIGTLSQDKFPQISFDLVFDKEFEL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 188; DB 5; Length 723; 23.5%; Pred. No. 4.2e-08; tive 53; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAME/KEY: Domain
LOCATION: 657.723
OTHER INFORMATION: /label- Mixed Charge
PCT-US92-11107-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 632..649
OTHER INFORMATION: /label- Basic II
                                                                                                                     ORGANISM: Drosophila melanogaster
INMEDIATE SOURCE:
CLONE: Drosophila SSRP (predicted)
                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 547..620
OTHER INFORMATION: /label- HMG-box
                                                                                                                                                                                                    NAME/KEY: Domain
LOCATION: 458..507
OTHER INFORMATION: /label- Acidic
                                                                                                                                                                                                                                                                                     NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label- Basic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 GGNNNKKPFNSGKQFGGSNNKGS 296
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SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76; Conservative
                                                                            MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Domain
                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                     FEATURE
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Sequence 4, Application US/08375300
Patent No. 5679566
GENERAL INFORMATION:
APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 EDNGDNEISKESQVDKDDNDNKDDEEEQGFTOEEDEEDDEEDDEEDDEEDDEE 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 SSSDCDTPPRQPPTSPISIGSSSPSECSWGDDTAMLVLLAEIAEEASKNEKECSENNQAG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1162;
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    Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEFONE. 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 180; DB 2; 27.8%; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                     ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-391-0523
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1162 antho acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 SSDDEDVPEAVPAPAPTAV-----
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 27.8%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-728-323A-2
TITLE OF INVENTION: En.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & E
                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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CITY: Boston
STATE: MA
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Matches
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APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GTKANVHFIGYKS----PNIEQDDFTSSDDED-----VPEAVPAPAPTAVTANGNAGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AVVKADTKPKAKPAEVKPAEEKPESDEEDESDEDESEEDDOSEKGMDVDEDDSDDEEE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ EETPKKPEPINKK----- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659 ESIDARKSEKVVASKIPVISKPVSVQRPLLLKKSEEPSSSKETYEELSKPKKIAFTFLTK 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 DDDDEEEEDSDSDLEYGGDLDADRDIEMKRMYEEYERKLKDEEERKAEEELERQFQKMMQ 658
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                                                                                                                                                                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 170; DB 1; Length 764; 25.3%; Pred. No. 1.5e-06; Itive 32; Mismatches 71; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                             71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                 NAME: FASSE, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (677)542-5070
TELEFAX: (617)542-8906
             APPLICATION NUMBER: US/08/375,300 FILING DATE: 20-JAN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/177,431 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/955,472
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Patent No. 6071700
                                                                                                                                                                          TELEX: 200154

TREATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 764 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
Matches 64; Conserv
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STREET: 44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL.
TITLE OF INVENTION: HEREROLOGOUS POLYPEPTIDE
TITLE OF INVENTION: NONSENSE-MEDIATED MRNA DECAY
TITLE OF INVENTION: FUNCTION
NUMBER OF SUCCESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
PRIOR APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
                                                                   07917/050001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9516930 GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUS
                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-9806
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
                     NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
ATTORNEY/AGENT INFORMATION:
                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-09-177-431-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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10.7%; Score 170; DB 5; Length 764;
Best Local Similarity 25.3%; Pred. No. 1.5e-06;
Matches 64; Conservative 32; Mismatches 71; Indels 86;
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046M01
TELECOMMUNICATION INFORMATION:
TELEPAX: 6617)542-5070
TELEPAX: 6617)542-5070
TELEX: 200154
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: Amino acid
STRANDEDNESS: single
TYPE: MOLECULE TYPE: protein
PCT-US95-16930-4
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Search completed: May 2, 2002, 22:08:42 Job time: 6118 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein · protein search, using sw model

Run on:

2, 2002, 22:07:30 ; Search time 205.36 Seconds (without alignments) 142.712 Million cell updates/sec

US-09-645-337-8 1589

Title: Perfect score: Sequence:

1 MEFWGVAVTPKNATKVTPEE.........KQFGGSNNKGSNKGKGKGRA 305

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | æ | | | SUMMARIES | |
|--------|-------|----------------|--------------------------|----|-----------|--------------------|
| Result | Score | Query Match | Query Match Length DB | DB | ID | Description |
| н | 1589 | 100.0 | 305 | ~ | T52287 | probable histone d |
| 7 | 543.5 | 34.2 | 307 | ~ | T04141 | histone deacetylas |
| e | 450.5 | 28.4 | 296 | ~ | T48401 | histone deacetylas |
| 4 | 311 | 19.6 | 412 | 7 | A55320 | immunophilin FKBP4 |
| S | 243 | 15.3 | 357 | 7 | JC4090 | FK506-binding 39k |
| 9 | 230 | • | 798 | ~ | T33022 | hypothetical prote |
| 7 | 215.5 | | 694 | - | DNCHNL | |
| 80 | 211.5 | 13.3 | 712 | 7 | JH0148 | nucleolin - rat |
| 6 | 207.5 | • | 611 | ~ | T06458 | nucleolin homolog |
| 10 | 206.5 | 13.0 | 707 | | DNMS | nucleolin · mouse |
| 11 | 206 | | 713 | 7 | A27441 | nucleolin - Chines |
| 12 | 202 | 12.9 | 707 | ~1 | A35804 | nucleolin - human |
| 13 | 200.5 | 12.6 | 281 | ~ | JC4295 | heat-shock protein |
| 14 | 196.5 | 12.4 | 635 | ~1 | T09648 | nucleolin homolog |
| 15 | 192.5 | • | 971 | 7 | T19431 | hypothetical prote |
| 16 | 188 | 11.8 | 723 | a | S33688 | hypothetical prote |
| 17 | 188 | • | 734 | 7 | B42680 | nucleolus-cytoplas |
| 18 | 186 | | 723 | | A48217 | single-strand DNA/ |
| 19 | 185 | 11.6 | 1151 | | T24541 | hypothetical prote |
| 20 | 183.5 | ٠ | 294 | | DNCHFM | nucleophosmin - ch |
| 21 | 182.5 | | 872 | | T18861 | probable peptide-a |
| 22 | 182.5 | • | 1187 | 7 | T46637 | transcription fact |
| 23 | 180.5 | | 374 | ~ | C88734 | protein F32E10.6 [|
| 24 | 180 | 11.3 | 1300 | ~ | T03166 | probable immediate |
| 25 | 178.5 | | 517 | ~ | S20248 | transcription fact |
| 56 | 177.5 | | 882 | ~ | G71608 | ATP-dept. acyl-CoA |
| 27 | 177.5 | 11.2 | 1473 | 7 | T13855 | suppressor of sabl |
| 28 | 177 | 11.1 | 644 | 7 | S55395 | neurofilament prot |
| 29 | 177 | 11.1 | 651 | 7 | S18874 | nucleolin - Africa |

| nucleolin - Africa hypothetical prote | myelin transcripti transcription fact | nypotnetical prote hypothetical prote zinc finger protei | peptidyl projyl ci nucleolar protein probable nuWl prot | glutamic acid-rich hypothetical prote | hypothetical prote NWD2 protein – yea NF-180 – sea lampr |
|--|--|--|---|--|--|
| S32644 T24169 T24166 | 130189 535551 | T08929 T25911 T46608 | T43536 I52858 A96527 | A54514 T28771 | T22330 S48244 I51116 |
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| 705 896 906 | 1182 | 753 211 1188 | 361 292 557 | 678 210 | 3498 1089 1110 |
| 11.11 | 11.1 | 11.0 | 10.9 | 10.8 10.8 | 10.7 10.7 10.7 |
| 177 176 176 | 176 | 174 | 173.5 172 172 | 172 | 170.5 170 170 |
| 30 31 | 1 m m 1 | 35 37 | 39 40 | 41 | 4 4 4 5 4 5 |

ALIGNMENTS

| RESULT 1 152287 probable histone deacetylase (EC 3.5.1) (imported) – Arabidopsis thallana | <pre>C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C:Accession: T52287</pre> | R.bangl, M.; Haas, H.; Loidl, P. submitted to the EMBL Data Library, January 1998 A.Descrintion: Arabidone's thallang community challenges that the second community of the comm | A: Reference number: 226016 A: Accession: T52287 | A;Status: preliminary; translated from GB/EMBL/DDBJ A;Noleule type: mRNA A;Noleule type: mRNA A;Noleule type: mRNA | A;Cross-references: EMBL:AF044914; PIDN:AAC02539.1 | A;Experimental source: cultivar Columbia C;Genetics: | A; Gene: HD2 | C;Keywords: hydrolase |
|---|--|--|---|--|--|---|--------------|-----------------------|
| RESULT T52287 probab | Č;Spe C;Dat C;Acc | R; Dan submi | A; Ref | A;Sta A;Mol | A; Cro | A; Exp C; Gen | A; Gen | C;Key |

Gaps .; 0 Ouery Match 100.0%; Score 1589; DB 2; Length 305; Best Local Similarity 100.0%; Pred. No. 6.6e-78; Matches 305; Conservative 0; Mismatches 0; Indels 0

ö 61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPATA 120 61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTA 120 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVDE 180 121 ò 셤 ò

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RESULT TO4141

| histone deacetylase (EC 3.5.1) HD2-p39, nucleolar - maize 2;Species: Zea mays (maize) | DD 55 IGTLEHEKPPOLSTEIVLERNFALSHTWKNGSYFFSGYKPEDLIDDOLEAAGF |
|---|--|
| C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C:Accession: T04141 | |
| RiLusser, A.; Brosch, G.; Loidl, A.; Haas, H.; Loidl, P. Science 277, 88-91, 1997 | 115 |
| A;Title: Identification of maize histone deacetylase HD2 as an acidic nucleolar phosphop K Reference number: 215237; WUID:97349336 | OY 169 DDDSEKGMDVDFDDSDDEFFEDSEDEEEETPKKPEPINKKRPNESVSK |
| *,Arcession: low-ta-: h.Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: mRNA | Db 161 GDEEEEKVTAESDSEEDDSSDEEDDSSEEETPKKPEEPKKRSAEPNSSK |
| A;Residues: 1-307 <lus> A;Cross-references: EMBL:U82815; NID:g2257755; PIDN:AAB63262.1; PID:g2257756 A;Experimental Source: strain Cuzco 251</lus> | OY 225 AKPAAAPASTPQKTEKKKGG-HTATPHPAKKGGKSPVNANOSPKSGGOSSGGNI |
| ., heywolds: Hydloldse | Qy 282 FNSGKQFG 289 |
| Query Match 34.2%; Score 543.5; DB 2; Length 307; Best Local Similarity 44.8%; Pred. No. 2.4e-22: | Db 264 KSAG-AFG 270 |
| Matches 130; Conservative 45; Mismatches 96; Indels 19; Gaps 11; | DECITE |
| OY 1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60 | RESULI 4 A55320 imminophilin FKBP46 – fall armyworm C;Species: Spodoptera frugiperda (fall armyworm) |
| Oy 61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTA 120 | C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change C.Accession: A55320 |
| DD 60 KNPHIQFDLIFDKEFELSHTSKTTSVFFTGYKVEQPFEEDEMDLDSEDEDEELNVPV 116 | R;Alnemri, E.S.; Fernandes-Alnemri, T.; Pomerenke, K.; Robertso, J. Biol. Chem. 269, 30828-30834, 1994 |
| QY 121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEBDESDESDESEEDDDSEKGMDV 178 | A:Ittle: FKBP46, a novel SI9 insect cell nuclear immunophilin t. A *Reference number: A55320; MUID:95074110 |
| Db 117 VKENGKADEKKQKSQEKAVAAPSKSSPDSKKSKDDDSDEDETDDSDEDTDDSDEGLSS 176 | A; Status: Assista |
| QY 179 DEDDSDDEEEDSEDEEEEETPKKPEPINKKRPNE-SVSKTPVSGKKAKPAAAPASTP 235 | A;MOLEGLIG TYPE: MKNA A:Residues: 1-412 <aln> A;Cross_references: GB:U15038; NID:g595844; PID:g595845</aln> |
| 236 | C.;Superiamily: yeast peptidyiptolyi isomerase FFK3; BRHP-type pr C;Reywords: nucleus; phosphoprotein F;234-371/Domain: RRB-type peptidyiprolyi isomerase homology < |
| Db 233 QKTGGKKGAAVHVATPHPAKGKTIVNNDKSVKSPKSAPKSGGSVPCKP 280 | |
| RESULT 3 | Query Match 19.6%; Score 311; DB 2; Length 412 Best Local Similarity 31.0%; Pred. No. 7.1e-10; Matches 100; Conservative 39; Mismatches 116; Indels |
| nistone deacetylase-like protein – Arabidopsis thaliana N.Alternate names: protein F17C15.160 | Qy 3 FWGVAVTP-KNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVI(|
| Species: Arabidopsis thaliana (mouse-ear cress) | |
| C;Accession: T48401 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000 | Oy 62 FPQISFDLVFDKEFELSH-SGTKANVHFIGYKSPNIEQDDFTSSDDKJVPE, |
| A. Accession: T48401 | Qy 119 TAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEED |
| 4,5cdus: preliminary Molecule type: DNA 8. Residinas: 1-306, ABV. | DD 119 AKNKRKLENANDATANKKAKPUKKAGKNSAPAAESUSDUDDEIXOLQKFILDGED |
| A.Cross references: EMBL:AL162506 F.Cross references: EMBL:AL162506 F.Cross references: cultivar Columbia; BAC clone F17C15 | |
| Venetics: | 179 |
| A;Introns: 5/1; 28/3; 93/3; 116/3; 164/3; 195/3; 227/1 A;Note: F17C15.160 | QY 212NESVSKTPVSGKKAKPAAAPASTPOKTEKKRG |
| Query Match 28.4%; Score 450.5; DB 2; Length 296; Best Local Similarity 38.3%; Pred. No. 2e-17; Matches 118; Conservative 39; Mismatches 94; Indels 57; Gaps 12; | QY 251 PAKKGGKSPVNANGSPK-SGGQS 272 : : : Db 287 PEAKKEEAPVEKKEKKQIAGGVS 309 |
| Oy 1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLV 53 | RESULT 5 |
| 54 IGTLSQDKFPQ1SFDLVFDKEFELSHSGTKANVHF1GYKSPN1EQDDFTSSDBED | CASSON STATES OF |
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merenke, K.; Robertson, N.M.; Dudley, K.; D
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ase FPR3; BKBP-type peptidylprolyl isomeras
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Feb-1995 #text_change 02-Sep-2000
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tches 116; Indels 68; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGDNDPCQVMVVVDGKNFLVCTLQKGK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVKSGESVVLSVTVGGAKLVIGTLSQDK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isomerase homology <PPI>
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14;

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A.Rolecule type: mRNA
A.Residues: 407-418, R., 420-519, T', 521-694 <BOR>
A.Cross-references: GB:M21791; NID:g212411; PIDN:AAA48983.1; PID:g212412
A.Cross-references: GB:M21791; NID:g212411; PIDN:AAA48983.1; PID:g212412
C.Comment: Phosphorylation of this protein by cdc2 kinase may contribute to the reorg C.Superfamily: nucleolin; ribonucleoprotein repeat homology
C.Superfamily: nucleolin; ribonucleoprotein repeat homology
C.Superfamily: nucleolin; ribonucleoprotein; nucleus; phosphoprotein; RNA binding F:1-2-4-7/Yomaan: acidic <ACI>
F:24-91/Region: nuclear location signal
F:254-262/Region: nuclear location signal
F:287-375/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Rosidues: 1-694 <MARZ>
A;Residues: 1-694 <MARZ>
R;Peter, M.; Nakagawa, J.; Doree, M.; Labbe, J.C.; Nigg, E.A.
Cell 60, 791-801, 1990
A;Tille: Identification of major nucleolar proteins as candidate mitotic substrates o
A;Reference number: A32725; MUID:90182668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EWBL:X17199; NID:g63710; PIDN:CAA35060.1; PID:g63711
R;Maridor, G.; Krek, W.; Nigg, E.A.
Bjochim. Biophys. Acta 1049, 126-133, 1990
A;Tile: Structure and developmental expression of chicken nucleolin and NO38: coordi A;Reference number: S10766; MUID:90304218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N'Alternate names: nucleolar protein C23
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S08414; S10766; A32725; I50397; B30099
R;Maridor, G.; Nigg, E.A.
Nucleic Acids Ree: 18, 126, 1990
A;Title: cDNA sequences of chicken nucleolin/C23 and N038/B23, two major nucleolar | A;Reference number: S08414; MUID:90206792
                                                                                                                                                                                                                                             ------PKKTAKSAIATAAE---DSDDDEEDDDEEEEE 273
                                                                                                                                                                                                                                                                                                      168 EDDDS---EKGMDVDEDDSDDDEEE----DSEDEEEETPKKPEPINKKRPNESVSKTPV 220
                                                                                                                                                                                                                                                                                                                                           48 GGAKLVIGTLSQDKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDE 107
                                                                                                                                                                          DVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 56-62;63-109;197-214 <PET>
K;Borer, R.A.; Lehner, C.F.; Eppenberger, H.M.; Nigg, E.A.
Cell 56, 379-390, 1989
A;Title: Major Nucleolar Proteins Shuttle between Nucleus and Cytoplasm.
A;Reference number: I50397; MUID:89119560
                                                                                                           181 GGSRVGF----SDKRKQYDSDGDDDEEEEVPKKKLATGTPFAKOTKP-VEDD--SGEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 SGKKAKPAAAPASTPQKTEKKKGGHTATPHPAKKGGKSPVNANQSPK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribonucleoprotein repeat homology <RRM4>RNA binding #status predicted <RNA4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonucleoprotein repeat homology <RRM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA binding *status predicted
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A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: translation not shown
                                                                                                                                                                                                                                       234 DEEESDEEPOP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-694 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S10766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleolin - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:373-448/Domain:
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F;555-631/Domain:
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                                                                                                                                      family of proteins that bind the immunosuppres
                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: FlyBase;FBgn0013269
C;Superfamily: yeast peptidylprolyl isomerase FPR3; BKBP-type peptidylprolyl isomerase
F;80-99/Region: acidic
F;252-357/Region: FK506 binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Cross-references: EMBL:AF047659; PIDN:AAC04430.1; GSPDB:GN00022; CESP:K07H8.10
A)Experimental source: strain Bristol N2; clone K07H8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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C;Date: 23-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000 C;Accession: JC4090
R;Theopold, U:; 2cto, L.D.; Hultmark, D.
Gene 156, 247-251, 1995
A;Title: FKBP39, a Drosophila member of a family of proteins that bind the i
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C:Date: 29-Oct 1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                 A:Title: FKBP39, a Drosophila member of a family of proteins that bind the A:Reference number: JC4090; MUID:95278752
A:Accession: JC4090
A:Molecule type: mRNA
A:Residues: 1-357 <THE>
A:Cross-references: EMBL:Z46894; NID:9600423; PIDN:CAA86996.1; PID:9600424 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 QNGVAKKEEAKQQQKKKE-----KPEAKKEQPKAKEPAKQQPASKDPRTITGGYKIVDQV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 PQISFDLVFDK-EFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 PQVALDLNFSKGDRIMFYTAGDASVSLLGY-----LHDIDSEDDEDDDQ------M 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDESS------E 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 TIENLLNSKAIKNSKKS------EDDEDENESGEEDEEDTDDDSQIIEEYESFLENGEE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 EDDDSEKGMDVDED--DSDDDEEEDSEDEE-EEETPKKPEPINKKRPNESVSKTPVSGKK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AKPAAAPASTPQKTEKKKGGHTATPHPAKKGGKSPVNANQSPKS-------268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 FWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQDKF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 --- GGOSSGG-----NNNKKPFNS---GKQF-----GGSNNKGSNKG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :252-357/Region: FK506 binding #status predicted
:269-316/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%; Score 243; DB 2; Length 357; 26.9%; Pred. No. 2.5e-06; tive 49; Mismatches 109; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 798;
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R;Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid K07HB.
A;Reference number: 221264
A;Accession: T33022
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31.7%; Pred. No. 2.7e-05;
tive 32; Mismatches 83
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A;Molecule type: DNA
A;Residues: 1-798 <FUL>
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A;Introns: 205/1; 308/3; 630/1; 773/3
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Best Local Similarity 31.7
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 95; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: K07H8.10
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F;575-639/Domain: ribonucleoprotein repeat homology <RRM4>
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C; Date: 31-Dec-1991 sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C; Accession: JH0148; A24088; I63130
R; Bourbon, H.M.; Amalric, F.
R; Bourbon, H.M.; Amalric, F.
A; F. Horleo, H.M.; Amalric, F.
A; F. Horleoin gene organization in rodents: highly conserved sequences within three A; Reference number: JH0148; MUID:90269607
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C;Comment: This protein is the major nucleolar-specific protein in eukaryotic exponentia
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C;Superfamily: nucleolin; ribonucleoprotein repeat homology
C;Keywords: DNA binding; nucleus
F;632-694/Domain: glycine/arginine-rich <GRR>
F;56,63,70,77,85/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status predi
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A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization A;Reference number: 148118; MUID:89121496
A;Accession: 163130
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A; Rote: the authors translated the initiation codon GTG for residue 1 as Val
A; Rote: the authors translated the initiation codon GTG for residue 1 as Val
B; Lischwe, M.A.; Cook, R.C.; Ahn, Y.S.; Yeoman, L.C.; Busch, H.
Biochemistry 24, 6025-6028, 1985
A; Title: Clustering of glycine and Ng.Ng-dimethylarginine in nucleolar protein C23.
A; Reference number: A24088; MUID:86104094
A; Accession: A24088
                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PAKKAATPAKKAVTPAKKAVAT----PAKKAVAPSPKKAAVVGKGAKNGKNAKKEESE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                  95 NIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPES 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 EEDEDDEEDDEEDEDEEEESDEEEEPAVPVK---PAAKKSAAAVPAKKPA-VVPA--KQES 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 EEDSEDEEEEETPKKPEPINK---KRPNESVSKTPVSGKKAKPAAAPAS-----TP 235
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                      4 LAKTPKNOMKOKKMAPPPKKVEESEEESSDLEESSGEEVMVPPKKQQKAAVTPAKKAAT 63
                                                                                                                                                                                                                                                                                                                           83;
                                                                                                            Length 694;
                                                                                                                                                                 Indels
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                                                                                                       13.6%; Score 215.5; DB 1; 28.1%; Pred. No. 0.00014; Live 32; Mismatches 102;
                                                                                                                                                                                                                 6 VAVIPKNATK----VIPEEDSLVHISQASLDCTVKSGESVVL-
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                                                                                                                                   Best Local Similarity 28.18
Matches 85; Conservative
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A; Residues: 'MV', 2-44 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 651-703 <LIS>
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                                                                                                            Query Match
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A40958; A40769; 184688
R;Bourbon, H.M.: Lapeyre, B.; Amalric, F.
J. Mol. Biol. 200, 627-638, 1988
A;Title: Structure of the mouse nucleolin gene. The complete sequence reveals that ea
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C:Species: Pisum sativum (graden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #Lext_change 08-Oct-1999
C:Accession: T06458
R:Tong, C.G.; Hsieh, H.L.; Blumenthal, S.; Reichler, S.; Balk, J.; Roux, S.J.
Submitted to the EMBL, Data Library, August 1995
A:Description: Molecular cloning and characterization of a cDNA encoding a nucleolin-A:Reference number: Z15692
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                                                                                                            97 EQUDETSSDDEDVPEAVPAPAPTAVTANCNACAAVVKADTKPKAKPAEVKPA-----E 149
                                                                                                                                                                   150 EEDEDDSDEDEEDEEDEFEPP------VKG-----VKPAKAAPAAPASEDED 190
                                                                                                                                                                                                                              EEEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQ-KTEKKKGGH 245
                                                                                                                                                                                                                                                                                                                                                                     A;Cross references: EMBL:L43510; NID:9940287; PIDN:AAA74208.1; PID:9940288 A;Experimental source: cv. Alaska C;Superfamily: nucleolin; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...---ESDDEDESEEDDDS----- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 ------EKGMDVDEDDSDDGEEDSEDEETPKKPEPINKKRPNESV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 TSKPSNGNKKPVTVSKKEDKMNVDKDSSDSDEESSDSEESESEDEPSKTPQKKTKDVEMI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 EQDDFTSSDDEDVPEAVP----APAPTAVTANGNAGAAVVKADTK-PKAK--PAEVKP- 147
                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 207.5; DB 2; Length 611; 30.9%; Pred. No. 0.00033; Live 24; Mismatches 54; Indels 65;
     Length 712;
                                                          Indels
     5
  Score 211.5; DB 2
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: T06458
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                       27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 -AEEKPES -----DEED ----
13.3%;
                                                       57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 TATPHPAKKGGKSP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 PITPFNLFIGNLNP 319
Query Match
Best Local Similarity
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Best Local Similarity
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Agrocession: A27441.
Asrocession: A27442.
Asrocession: A24808.
Asrocessi
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C;Date: 23-Oct-1990 #text_change 23-Jul-1999
C;Date: 23-Oct-1990 #sequence. Reacensis Response 23-Jul-1999
C;Accession: A35804; S04631; A48138; A5596
R;Srivastava, M.: McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
J. Biol. Chem. 265, 14922-14931, 1990
J. Filtle: Genomic organization and chromosomal localization of the human nucleolin gen
A;Reference number: A35804; MUID:90368666
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R;Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999 C;Accession: A27441; A24808; A24070 R;Lapeyre, B.; Bourbon, H.; Amalric, F. Proc. Natl. Acad. Sci. U.S.A. 84, 1472-1476, 1987 A;Title: Nucleolin, the major nucleolar protein of growing eukaryotic cells: A;Reference number: A27441; MUID:87175501
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Best Local Similarity 23.2%; Pred. No. 0.00046;
Matches 66; Conservative 31; Mismatches 81;
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A;Molecule type: mRNA
A;Residues: 179-238 <LA3>
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A; Residues: 1-707 <SRI>
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C:Reywords: DNA binding; duplication; nucleus; phosphoprotein; RNA binding; transcriptic
F:310-375/Domain: ribonucleoprotein repeat homology <RRM1>
F:311-316/Region: RNA-binding RNP2 motif
F:349-356/Region: RNA-binding RNP1 motif
                                                                                                                                                                                A;Cross-references: GB:X07699; NID:953453; PIDN:CAA30538.1; PID:953454
R;Pasternack, M.S.; Bleier, K.J.; McInerney, T.N.
J Blol. (Dhm. 266, 14703.14708, 1991
A;Title: Granzyme A binding to target cell proteins. Granzyme A binds to and cleaves nucleic mumber: A40769; MUID:91317840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Wolecule type: protein
A; Residues: 2-20, X', Z2-4 < PAS>
R; Residues: 2-20, X', Z2-4 < PAS>
R; Yang, T. H.; Tsai, W. H.; Lee, Y. M.; Lei, H. Y.; Lai, M. Y.; Chen, D. S.; Yeh, N. H.; Lee, S Mol. Cell. Biol. 14, 6068-6074, 1994
A; Title: Purification and characterization of nucleolin and its identification as a tran A; Reference number: A56240; MUID: 94344117
A; Accession: A56240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosa-references: GB:M22089; NID:q200111; PIDN:AAA39841.1; PID:q554246
C;Comment: This housekeeping protein is involved in the synthesis, packaging, and matura
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A:Introns: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; 566/1; 608
C;Superfamily: nucleoiin; ribonucleoprotein remain human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 68, 73-84, 1988
A:Title: Sequence and structure of the nucleolin promoter in rodents: Characterization
A:Reference number: 148118; MUID:89121496
A:Recession: 184688
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N;Alternate names: nonchromosomal protein C23; nucleolar protein C23
C;Species: Cricetulus griseus (Chinese hamster)
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F;571-576/Region: RNA-binding RNP2 motif
F;607-614/Region: RNA-binding RNP1 motif
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A; Reference number: A29958; MUID:88316930
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F;524-531/Region: RNA-binding RNP1 motif
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A;Residues: 2-19;558-567 <YAN>
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                                                                                                                                                    A; Residues: 1-707 <BOU>
                                                                                                        A; Molecule type: DNA
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                                            Accession: A29958
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Matches 6
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A; Residues: 1-281 <DEM>
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                                                                                            A;Molecule type: mRNA
A;Residues: 1-707 <SR2>
R;Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
Mol. Cell. Biol. 13, 4301-4310, 1993
A;Tille: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G) and
A;Reference number: A48138; MUID:93309464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 APTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEE----- 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 EPAAMKA---AAAA------PASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPA
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Wolecule type: protein
A;Residues: 231-236;349-362;399-403;458-461;655-656,'X',658-660 <JOR>
A;Exporimental source: surface-labelled HeLa cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cikeywords: DNA binding; nucleous; nucleus; phosphoprotein; 18;308-373/Domain: ribonucleoprotein repeat homology <RRM1> F;308-456/Domain: ribonucleoprotein repeat homology <RRM1> F;487-556/Domain: ribonucleoprotein repeat homology <RRM3> F;573-634/Domain: ribonucleoprotein repeat homology <RRM3>
                                                                                                                                                                                                                                                                            A:Experimental source: HeLa cell nuclei
A:Note: sequence extracted from NCBI backbone (NCBIP:134645)
                  A;Title: Cloning and sequencing of the human nucleolin cDNA.
A;Reference number: S04631; MUID:89290043
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A;Gene: Apple: GDB:125908; OMIM:164035
A;Map position: 2q12-2qter
A;Map position: 2q12-2qter
C:Superfamily: nucleolin; ribonucleoprotein repeat homology
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                                                                           A; Status: not compared with conceptual translation
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Biochemistry 33, 14696-14706, 1994
Lett. 250, 99-105, 1989
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Rest Local Similarity
Local 74; Conserva
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A; Residues: 458-474 <ISH>
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                                                         A; Accession: S04631
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RiBoegre, L.; Jonak, C.; Mink, M.; Meskiene, I.; Traas, J.; Ha, D.T.C.; Swoboda, I.; Plant Cell B, 417-428, 1996
A;Title: Developmental and cell cycle regulation of Alfalia nucMs1 a plant homolog of A;Reference number: 216796; MUID:96361876
A;Reference number: 2009648
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: nuWl protein
C;Specise: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAKPAAAPASTPOKTE------KRKGGHTATPHPAKKGGKSPVNANQSP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 KSPNIEQDDFTSSDDEDVPEAVPA----PAPTAVTANGNAGAAVVKA----DFKPKAKPA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --EDESEEDDDSEKGMDVDEDDSDDD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 AVAKKSKKDSSDSDDEDDDSSSDEDKKPVASKKEVSESESDSSDDHK-MNIDKDSSDSD 329
                                                                                                                                                                                                                                                                                                                                                                          61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VTANG------RAGAAVVKADTKPKAKPAEVKPAE-----EKPESDEEDESDDE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 DESEEDDDSEKGMDVDEDDSDDDEEEDSEDEEEETPKKPEPINKKRPNESVSKTPVSGK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKTPEPKKVPEPKKEGVKQPTQPQQKKAAAQQPEKANNKPAAASPAKPQNNGSKNAPKQP 252
                                                                                                                                                                                                                                                                                                                                                                                                             1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60
  PID:9662359
                                                                                                                                                                                                                                                                                                   2 MQFFGTIVTKEBPVNLELDEGDIFHLTKAJJHPKSQGKGKVYJTA-----VISLMEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPOKTEKKK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 635;
                                                                                                                                          Length 281;
                                                                                                                                                                                                  49; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
A;Cross-references: GB:L39778; NID:9662358; PIDN:AAA99510.1; C;Comment: This protein has roles in growth, development and C;Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: nucleolin; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                             DB 2;
                                                                                                                                          Score 200.5; DB 2
Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 196.5; DB 31.8%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 QQQQQSPAKNNNKRPQNQNE-----NNKKQK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 KSGGQS-SGGNNNKKPFNSGKQFGGSNNKGSNK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                       12.6%;
21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleolin homolog nuMl - alfalfa
                                                                                                                                                                       Best_Local Similarity 21.69
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 EVKPAEEKPESDEEDESDD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-635 <BOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 56;
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: nuMl
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11;
hypothetical protein C25A1.10 - Caenorhabditis elegans
C; Species: Cacnorhabditis elegans
C; Species: Cacnorhabditis elegans
C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C; Accession: T19431
R; Mortimore, B.
submitted to the EMBL Data Library, October 1996
A; Reference number: Z19124
A; Reference number: Z19124
A; Scession: T19431
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Schoule type: DNA
A; Molecule type: DNA
A; Residues: 1-971 < WILL>
A; Cross-references: EMBL: Z81038; PIDN: CAB02755.1; GSPDB: GN00019; CESP: C25A1.10
A; Cross-references: elmbL: Z81038; PIDN: CAB02755.1; GSPDB: GN00019; CESP: C25A1.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EEDSEDEEEETPK-----KPEPINKKR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 PNESVSKTPVSGKKAKPAAAPAS---TPQKTEK------KKGGHTATPHPA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 ESSSDS----SDDEKKPVAKPTSAKATPKPAAKKADLSSDFSDDEAPAKKTPAKAAPKPA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 EEDESDDE------KGMDV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 SSDDEDVPEAVPAPA---PTAVTANGNAGAAVVKADTKPKAKP----AEVKPAEEKPESD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 12.1%; Score 192.5; DB 2; Length 971; Best Local Similarity 25.7%; Pred. No. 0.0033; Matches 74; Conservative 27; Mismatches 90; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| :: | :: | 581 SKRAESSSDSSDDEKPAAKSTPAKTTPKP--TAKKAASSSDSSDDEK 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 KKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSNKGK 300
                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
A;Introns: 38/3; 92/3; 201/3; 919/3
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: May 2, 2002, 22:07:31
Job time: 6679 sec
                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: CESP:C25A1.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 DEDDSDDDE-
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GenCore version 4.5
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OM protein - protein search, using sw model

May 2, 2002, 22:31:08; Search time 36 81 Seconds (without alignments) 320.822 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-645-337-8 1589 1 MEFWGVAVTPKNATKVTPEE......KQFGGSNNKGSNKGKGKGRA 305

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 segs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | • | | | SUMMARIES | |
|--------|-------|-------|--------|-------------|-------------|--------------------|
| Result | | Query | | | | |
| NO. | Score | Match | Length | DB | QI | Description |
| -1 | 311 | 19.6 | 412 | - | FKB4_SPOFR | 026486 spodoptera |
| 71 | 240 | 15.1 | 357 | ٦ | FKB4_DROME | - |
| æ | 215.5 | 13.6 | 694 | 7 | NUCL_CHICK | |
| 4 | 211.5 | 13.3 | 712 | - | NUCL_RAT | P13383 rattus norv |
| 2 | 208 | 13.1 | 411 | Н | MP62_LYTPI | P91753 lytechinus |
| ø | 206.5 | 13.0 | 206 | - | NUCL_MOUSE | |
| 7 | 206 | 13.0 | 713 | Н | NUCL_MESAU | P08199 mesocricetu |
| œ | 205 | ٠ | 206 | - | NUCL_HUMAN | P19338 homo sapien |
| σ | 200.5 | 12.6 | 281 | _ | HS32_DICDI | 60 |
| 10 | 188 | 11.8 | 704 | - | NP14_RAT | P41777 rattus norv |
| 11 | 188 | 11.8 | 723 | - | SSRP_DROME | |
| 12 | 183.5 | 11.5 | 294 | - | NPM_CHICK | • |
| 13 | 178.5 | 11.2 | 517 | 7 | T2FA_HUMAN | |
| 14 | 177 | 11.1 | 644 | - | NFM_RABIT | P54938 oryctolagus |
| 15 | 177 | 11.1 | 650 | - | NUCL_XENLA | |
| 16 | | | 524 | _ | T2FA_XENLA | |
| 17 | 173.5 | 10.9 | | - | FKB4_SCHPO | 074191 schizosacch |
| 18 | 172 | 10.8 | | - | NPM_MOUSE | Q61937 mus musculu |
| 19 | 172 | 10.8 | | - | GARP_PLAFF | P13816 plasmodium |
| 20 | 170 | 10.7 | 1089 | | NMD2_YEAST | P38798 saccharomyc |
| 21 | 169.5 | 10.7 | 543 | - | TLP1_MOUSE | Q9z273 mus musculu |
| 22 | 169 | 10.6 | | - | NPM_RAT | P13084 rattus norv |
| 23 | 168.5 | 10.6 | | - | NPM_XENLA | |
| 24 | 168.5 | 10.6 | | - | NP14_HUMAN | Q14978 homo sapien |
| 25 | 168 | 10.6 | | | FKB3_YEAST | P38911 saccharomyc |
| 56 | 168 | 10.6 | _ | - | Y EMA_DROME | P25992 drosophila |
| 27 | 167.5 | 10.5 | 915 | | NFM_HUMAN | P07197 homo sapien |
| 28 | 167 | 10.5 | _ | | TRP_DROME | P19334 drosophila |
| 29 | 166 | 10.4 | 304 | | CEC1_CAEEL | |
| 30 | 166 | 10.4 | 542 | - | TUL1_HUMAN | 000294 homo sapien |
| 31 | 164.5 | 10.4 | | - | | Q23525 caenorhabdi |
| 32 | 164.5 | 10.4 | | _ | | |
| 33 | 162.5 | 10.2 | 1109 | | TCF8_RAT | Q62947 rattus norv |

| | | | | | | | | | | P41073 drosophila | |
|------------|----------|------------|-----------|------------|-----------|-----------|---------|------------|------------|-------------------|-----------|
| MAZ4_SCHCO | YKR4_EBV | SIS2_YEAST | NFH_HUMAN | SERA ENTHI | NPM_HUMAN | AF4_MOUSE | NFM_RAT | MRSP_STAAU | HMCU_DROME | PEP_DROME | NFM_MOUSE |
| _ | - | - | - | - | - | _ | 7 | | ч | Н | 7 |
| 940 | 217 | 562 | 1020 | 233 | 294 | 1217 | 845 | 1637 | 2175 | 716 | 848 |
| 10.2 | 10.2 | 10.2 | 10.2 | 10.1 | 10.1 | 10.1 | 10.1 | 10.1 | 10.1 | 10.0 | 6.6 |
| | | Ŋ | 3. | 191 | 0.5 | 0.5 | 160 | 160 | 160 | 8.5 | 158 |
| 162 | 161.5 | 161 | 161 | | 16 | 16 | | | | 7 | |

ALIGNMENTS

| | ID FKB4_SPOFR | STANDARD; | ARD; | PRT; | 412 | AA. | | | |
|--------|---|-----------------------|--|---|---------------|-------------------------------|-------------------|------------------|-----------------------------|
| | 026486; | | | | | | | | |
| | | | 35, created) 35, Last sequence update) | neuce n | ıpdat | (a) | | | |
| | 15-JUL-1999 (Rel. 38, Last annotation update) 46 kDa FK506-binding nuclear protein (PeptidvI-prolvI | (Rel. 38, -binding | 38, Last ann ing nuclear p | annotation update) ar protein (Peptidv | ded) | ate) tidvl-p | rolvl | cis-trans | 50 |
| | isomerase) (| PPiase) | (PPiase) (EC 5.2.1.8). | 8). | | | | | <u>!</u> |
| | | rugiperda | frugiperda (Fall armyworm). | myworm) | · | | | | |
| | Eukaryota; m Ptervoota: N | etazoa; / eoptera: | Metazoa; Arthropoda; Itacheata; Hexapoda; Insecta; Neobtera: Endoptervoota: Lebidoptera: Glossata: Ditrysia | ; Trach gota: I | leata enid | ; Hexap | oda; II Glossa | secta; | trvaia. |
| | | Noctuidae | Amphipy | rinae; | Spod | optera, | | 1 | 1242143 |
| | NCBI_TaxID=7108; | 108; | | | • | • | | | |
| | [1] | | | | | | | | |
| | SEQUENCE FROM N.A. MEDLINE=95074110: PubMed=7527037: | M N.A. 4110: Pul | Med=75270 | 37: | | | | | |
| | Alnemri E.S. | , Fernand | E.S., Fernandes-Alnemri T | 1 T. | отег | Pomerenke K., | | Robertson N | N. H. |
| | Dudley K., Dubois G.C., Litwack G.; | ubois G. | C., Litwac | K G.: | | | | | |
| | *FKBP46, a novel Sf9 inse | ovel Sf9 | insect ce | ll nucl | ear | immunophilin that | hilin | | forms a |
| | protein-Kinase | se compie | .x.; | . 1001. | | | | | |
| | -I- FIINCTION | MI. 209:30 | TOI, CHEMI, 207:30020-30034(1994). PHYPTION: BINDS WO, AND IS INHIBITED BY EXECS AND BADANNIN | TNHTBI | TED. | RV FK50 | AND 1 | ONNAGAG | SUNTE NI |
| ဗ္ဗ | | DOUBLE-STRANDED DNA | NA IN VIT | RO. PPI | ASES | ACCELE | RATE PI | ROTEIN | |
| ပ္ပ | -!- CATALYTI | C ACTIVIT | CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC | ANS ISC | MERI | ZATION | OF PRO | LINE IM | IDIC |
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| | -!- SIMILARI | TY: BELO! | SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. | FKBP-1 | YPE | PPIASE | FAMILY | | |
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| | Into Swiss-rword entry is copyright. It is produced unrough a collaboration between the Swiss Institute of Richformatics and the EMMI outstation | Swiss In | stitute o | f Rioir | form | produc | and the | ough a | COLLABOR |
| ខួ | the European Bioinformatics Institute. | Bioinfo | rmatics In | stitute | J . | There ar | are no | restrictions | tions on |
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| DR | EMBL; U15038 | ; AAA589 | 52.1; | | | | | | |
| Z G | HSSP; P20071; 1FKJ. | ; 1FKJ. | | | | | | | |
| ¥ 6 | InterPro; IF | R0011/9; | FKBP_PPIa | se. | | | | | |
| | Promi; Prouds | 4; FRBP; | I. | | 9 | ç | | | |
| | PROSITE; PSOU403; FABF_FIASE_1; FALSE_NEG PROSITE: PSOU454: FKRP PPIASE 2: 1 | 0455; FRI | AP PPIASE | 2: 1 FALS | 7. 1.2. | <u>.</u> | | | |
| | | 0059; FK | PS50059; FKBP PPIASE 3: | | | | | | |
| 3 | se, | Rotamase: Nuclear | Nuclear p | rotein: | ON'S | -bindin | a: Phos | sphoryl | ation. |
| | | 91 1 | 112 A | SP/GLU- | RICH | ASP/GLU-RICH (HIGHLY ACIDIC). | Y ACID: | IC). | |
| | DOMAIN | | | LYS-RICH (BASIC) | H (BA | Sic). | | | |
| | DOMAIN | | | SP/GLU- | RICH | ASP/GLU-RICH (HIGHLY ACIDIC) | Y ACID: | . (DI | |
| | DOMAIN | | | LYS-RICH (BASIC). | 4 (BA | SIC). | | | |
| | DOMAIN | .7 728 | 412 D | PIASE | FKRD | PPIASE, FKBP-TYPE. | | | |
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Query Match

19.6%; Score 311; DB 1; Length 412;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams W.D., Celnikor S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R. George R.A., Lewis S.E., Fichards S., Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Brandon R.C., Bayerre E.G., Helt G., Nelson C.R., Miklos G.L.G.,
R. Ballew R.M., Basu A., Baxendale J., Bayraktaroqlu L., Beasley E.M.,
R. Beson K.Y., Benos P.P., Bhandari D., Bolshakov S.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
R. Cherry J.W., Cawley S., Dahike C., Davenport L.B., Davies P.,
R.A. Cherry J.W., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
R. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R. Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
R. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera; Endopteryqota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                            62 FPQISFDLVFDKEFELSH-SCTKANVHFIGYKSPNIEQD--DFTSSDDEDVPEAVPAPAP 118
                                                                                                                                                                                    59 IIQVPLDLYFKSGDSVSFLTNGKCNVHLTGYLDPEFEEDLEDEEEAEEEEEEEEAPPLVP 118
                                                                                                                                                                                                                        119 T---AVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEED------ESDDED 164
                                                                                                                                                                                                                                                                  119 AKNKRKLENANDATANKKAKPDKKAGKNSAPAAESDSDDDDEDQLQKFLDCEDIDTDEND 178
                                                             3 FWGVAVTP-KNATKVIPEEDSLVHISQASLDCIVKSGESVVLSVTVGGAKLVIGTLSQDK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theopold U., Dal Zotto L., Hultmark D., "FKBP39, a Drosophila member of a family of proteins that bind the
                                                                                                   2 FWGLIMEPNKRYTQVV---EKPFHISQAAMDISTGDNDPCQVMVVVDGKNFLVCTLQKGK
                                                                                                                                                                                                                                                                                                                                                   ESFKMNTSAEGDUSDEEDDDDEDEEDEDDDDDDDEEBEBARK - - - - KKKQPAAEQDSTLD
                                                                                                                                                                                                                                                                                                                                                                                           --NESV--SKTPVSGK------KAKPAAAPASTP-----QKTEKKGGHTATPH
                                                                                                                                                                                                                                                                                                                                                                                                                 FKB4_DROME STANDARD, PRT; 357 AA.
P54397, 09VRB9.
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
39 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans isomerase) (Pplace) EC 5.2.1.8).
FK506-BPI OR FKBP39 or CG6226.
                                                                                                                                                                                                                                                                                                             ESEEDDDSEKGMDVDEDDSDDDEE----EDSEDEEEETPKKPEPINKKRP----
                       Indels
                   116;
  2.8e-10;
                       Mismatches
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2
    Pred.
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MEDLINE-95278752; PubMed-7538962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 PAKKGCKSPVNANQSPK-SGGQS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAKKEEAPVEKKEKKOIAGGVS 309
                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fmmunosuppressive drug FK506.";
Gene 156:247-251(1995).
  31.0%;
                     Conservative
Best Local Similarity
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                     Matches
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Aliali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Liang Y., Lia Z.,
Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Aclascolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Raine B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Ray Evirskas R., Tector C., Trnner R., Wenter F., Wang A.H.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
Rh Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rh Grome sequence of Drosophila melanogaster.";
Science 287:2185-2195-2000).
C. -- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS: FKBP506
MAY FUNCTION: PIASES ACCELERATE THE FOLDING OF PROTEINS FKBP506
MAY FUNCTION: PLANSWING TARANSDUCTION CASCADE DURING EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WITH HIGHEST EXPRESSION IN EARLY EMBRYO.
SIMILARITY: BELONGS TO THE FYBP-TYPE PPIASE FAMILY.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --E 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 FWGLNMKPER--KYSQTIIKSFHISGVALD----KGQEAKI,YLAAEKQEYIVATVTK-AI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- DEVELOPMENTAL STAGE: EXPRESSED DURING ALL STAGES OF DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED, HIGHEST LEVELS IN
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EFOAB7831738BB30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASP/GLU-RICH (HIGHLY ASP/GLU-RICH (HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 240; DB 1;
Pred. No. 1.4e-06;
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PPIASE, FKBP-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase; Rotamase; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P27124; iROT.
Flybase; FGGN00113269; FK506-bpl.
InterPro; IPR001179; FKBP_PPlase-
Pfam; PF00254; FKBP, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus galius (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                          102 TIENLLNSKAIKNSKKS-----EDDEDENESGEEDEEDTDDDSQIIEEYESFLENGEE 154
                                      168 EDDDSEKGMDVDED--DSDDDEEEDSEDEE-EEETPKKPEPINKKRPNESVSKTPVSGKK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANOCLEGOLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDERSATION BY BINDING TO HISTOME HI. IT IS THOUGHT TO PLAY A DECONDERSATION BY BINDING TO HISTOME HI. IT IS THOUGHT TO PLAY A SUBCELIULAR INCATION: NUCLEARIS, NUCLEARIS, SEMBLY. SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE-99304215; PubMed-2114180; Maridor G., Krek W., Nigg E.A.; "Structure and developmental expression of chicken nucleolin and "Structure and developmental expression of two abundant non-ribosomal nucleolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89119560; PubMed-2914325; Borer R.A., Lehner C.F., Eppenberger H.M., Nigg E.A.; "Major nucleolar proteins shuttle between nucleus and cytoplasm."; Cell 56:379-390(1989).
                                                                                                                                        FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'cDNA sequences of chicken nucleolin/C23 and NO38/B23, two major
                                                                                                                                                                                          269 ---GGQSSGG-----GGNNKRPINS---GKQF-----GGSNNKGSNKG 299
                                                                                                                                                                                                                260 VGKGEEAKQCKRVSVYYIGRLQSNNKTFDSLLKGKPFKFALGGGEVIKGWDVG 312
                                                                                                                225 AKPAAAPASTPOKTEKKKGGHTATPHPAKKGGKSPVNANQSPKS-
                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Nucleolin (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1049:126-133(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleolar proteins.";
Nucleic Acids Res. 18:1286-1286(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-90206792; PubMed-2320420;
Maridor G., Nigg E.A.;
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InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
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                                                                                                                                                                                                                                                                                                                              STANDARD;
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P15771;
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 NIEGDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPES 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEEDESDDEDESEEDDDSE-KGMDV------DEDDSDDB 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                6 VAVTPKNATK----VTPEEDSLVHISQASLDCTVKSGESVVL-----SVT------ 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bourbon H.-M., Amalric F.; "Nucleolin gene organization in rodents: highly conserved sequences within three of the 13 introns.";
PROSITE; PS00030; RRM_RNP_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                              47 -------VGGAKLVIGTLSQDKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSP
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                  DB 1; Length 694;
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N -> T (IN REF. 3).
7996C504BE9459A1 CRC64;
                                              ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
                                                                                RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
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(BY
                                                                                                                                                                                                                                                                                                              13.6%; Score 215.5; DB 1; 28.1%; Pred. No. 5.2e-05; live 32; Mismatches 102;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nucleolin (Protein C23).
                                                                                                                                 ARG/GLY/PHE-RICH
                                                                                                                                                                                                                PHOSPHORYLATION
PHOSPHORYLATION
PHOSPHORYLATION
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                                                                                                                                                                                                                                                                            75640 MW;
                                                                                                                                                                                                                                                                                                                Ouery Match 13.6%
Best Local Similarity 28.1%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCL OR NUC.
Rattus norvegicus (Rat).
                                                                                                                                         90
61
68
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                                                                                                                                                                                                                                                                             694 AA;
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CONFLICT
SEQUENCE
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARG/GLY/PHE-RICH.
B X 8 AA TANDEM REPEATS OF X-T-P-X-K-K-X-X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRW_RN_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat; RNA-binding.
                                                                                                       -i- FUNCTION: NUCLECLIN IS THE MAJOR NUCLECLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLECLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE HI. IT IS THOUGHT TO PLAY ROLE IN PRE-RRAM TRANSCRIPTION AND RIBOSOME ASSEMBLY.
-i- SUBCELLULAR LOCATION: NUCLEAR; NUCLECLUS.
                                      MEDLINE-89121496; PubMed-2906027;
Bourbon H.-W., Prudhomme M., Amalric F.;
Sequence and structure of the nucleolin promoter in rodents:
characterization of a strikingly conserved CpG island.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKPESDEEDESDDEDESEEDDDSEKGMDV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 29.4%; Pred. No. 8.7e-
Conservative 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.3%; Score 211.5; 29.4%; Pred. No. 8.7
                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              EMBL; M55015; AAA41732.1; JOINED.
EMBL; M55017; AAA41732.1; JOINED.
EMBL; M55020; AAA41732.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77016 MW;
                                                                                                                                                                                                                                                                                                                                  EMBL; M55022; AAA41732.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M22090; AAA41733.1; -.
                           SEQUENCE OF 1-44 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000504; RRM. Pfam; PF00076; rrm; 4.
Gene 88:187-196(1990).
                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JH0148; JH0148.
HSSP; P09651; 1HA1.
                                                                                               Gene 68:73-84(1988)
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Local Sun-
57;
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26 GKDFEGAEA - - YEVGDEDLEDEDEGEEDFEREETPKKGSPKRIVKKIAAVKGRMKGKGDE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 IEQDDFTSSDDEDVPEAVPA-----PAPTAVTANGNAG--AAVVKADTKPKAKP---AE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97; Indels 138; Caps
                                                                                                                                                                                                                                                         Mitotic apparatus protein P62.
Lytechinus pictus (Painted sea urchin).
Eukaryota: Metazoa: Echinodermata: Eleutherozoa: Echinozoa:
Echinoidea: Euechinoidea: Echinacea: Temnopleuroida: Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 FWGATLSKDKKIFKWDPESDFLDDEDDDEEDSISHFLFLKQAVLGVNAKDDDRNVIEVET 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                     required for mitotic progression.";
J. Biol. Chem. 272:3606-3614(1997).
-i- FUNCTION: REQUIRED FOR MITOTIC PROGRESSION. BINDS TO CHROMATIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 ---SGESVV---LSVTVG------CAKLVIGTLSQDKFPQ1SFDLVFDKEF
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-97166213; PubMed-9013612;
Ye X., Sloboda R.D.;
"Molecular characterization of p62, a mitolic apparatus protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 208; DB 1; Length 411;
Pred. No. 8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D2DE04293C362254 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- PTM: PHOSPHORYLATED BY CAM-KINASE II IN VITRO.
-i- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
                                                                                                                                                                                                                            39, Last sequence update)
39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; VOCCO, MINICOLEOPLASMIN.
Pfam; PP03066; Nucleoplasmin; 1.
Nuclear protein; Phosphorylation; Mitosis.
NAMMIN 147 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46385 MW;
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                                                  246 TATPHPAKKGGKSP 259
                                                                                    306 PTTPFNLFIGNLNP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-7653;
                                                                                                                                                                      MP62_LYTPI
                                                                                                                                                                                                                                                                                                                                Lytechinus
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SEQUENCE
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                                                       241 NCHAIDDDEDDEEDEDYKVGDEEEEEEATSGEEEEEEEBEEEEEEDDEEMALG-DDDDEDD 299
                                                                                                                                                   145 VKPAEEKPESDEED--------ESDDEDESEEDDDSEKGMDVDEDDSDD 185
                                                                                                                 186 DEEE-----DSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bourbon H.M., Prudhomme M., Amalric F.; "Sequence and structure of the nucleolin promoter in rodents: Characterization of a strikingly conserved CpG island."; Gene 68:73-84(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCL_MOUSE STANDARD; PRT; 706 AA. P09405; 061991; 01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Nucleolin (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-44 FROM N.A. MEDLINE-89121496; PubMed-2906027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-23.
MEDLINE-91317840; PubMed-1860869;
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InterPro; IPR000504; RRM.
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SMART; SM00360; RRM; 4.
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NUCL_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             150 EEDEDDSDEDEDEEEDEFEPP------IVKG-VKP-AKAAPAAPASEDEEDDE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lapeyre B., Bourbon H., Amalric F.; "Nucleolin, the major nucleolar protein of growing eukaryotic cells: an unusual protein structure revealed by the nucleotide sequence."; proc. Natl. Acad. Sci. U.S.A. 84:1472-1476(1987).
                                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY).

8 X 8 AA TANDEM REPEATS OF X-T-P-X-K-K-X-X.
 ; RRM; 4.
; RRM_RNP_1; 3.
Phosphorylation; Methylation; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                      Length 706;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                             (ACIDIC).
(ACIDIC).
(ACIDIC).
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                                                            ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARG/GLY/PHE-RICH.
                                                                                                                                                                                                                                                                                                                                                                   13.0%; Score 206.5; DB 1; 33.0%; Pred. No. 0.00016; tive 15; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Nucleolin (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 AA.
                                                                                                                                                                                                                                                                              (INCOMPLETE)
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                                                                                                                                                                                                                                                                          103 5.111 6.112 6.126 7.134 8.76592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GCHTATPHPAKKGGKSP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GSEPITPFNLFIGNLNP 317
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                              64
81
89
97
PROSITE; PS50102; R
PROSITE; PS00030; R
Nuclear protein; Ph
RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                706 AA;
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FUNCTION.
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                                                 INIT_MET
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MOD_RES
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REPEAT
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ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARM-BINDING (RRM) 4.
8 X 8 AA TANDEM REPEATS OF X-T-P-X-K-K-
                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0102; RRM; 4. NOSOTE; PS00030; RRM RNP_1; 3. Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat; RNA-binding.
                                                        EUT. J. Biochem. 175:525-530(1988).
-1- FUNCTION: NUCLEDIAN IS THE MAJOR NUCLEDLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEDIAR CHROMATIN AND PRENIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE HI. IT IS THOUGHT TO PLAY ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME ASSEMBLY.
            Brard M.S., Belenguer P., Caizergues-Ferrer M., Pantaloni A.,
Nmalric F.;
                                  "A major nucleolar protein, nucleolin, induces chromatin decondensation by binding to histone H1.";
Eur. J. Biochem. 175:525-530(1988).
                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79DDCF724CED7DB4 CRC64;
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Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
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694
713 AA;
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13.0%; Score 206; DB 1; Length 713; 23.2%; Pred. No. 0.00017; Live 31; Mismatches 81; Indels 1
     Query Match
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-- 117 Gaps

- AVPAPA-----

81; Indels 106;

Conservative

Best Local Similarity Matches 66; Conserv

Matches

97 RODDFTSSDDEDVPE----

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                                                                                        94 KAVTPAKAVATPGKKGATQAKALVATPGKKGAVTPAKGAKNGKNAKKEDSDEDEDDDDDDE 153
                                                                                                                                                 166 SEEDDDSEKGMDVDEDD------SDDDEEEDSEDEEEEFFFKKPEP 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleolin gene.";
J. Biol. Chem. 265:14922-14931(1990).
J. Biol. Chem. 265:1017 IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING
-!- FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING
EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR
CHROMATIN AND PRERIEDSORMAL PARTICLES. IT INDUCES CHROMATIN
DECONDENSATION BY BINDING TO HISTONE HI. IT IS THOUGHT TO PLAY A
|::| :| :: :|: 34 EEEDDSSGEEVVIPQKKGKKATATPAKKVVVSQTKKVAVPTPAKKAAVTPGKKAAATPAK 93
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                                                                                                                                                                          ----PTAVTANGNAGAAVVKADTKPKAKPAEVKPAE-----EKPESDEEDESDDEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-!- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89290043; PubMed-2737305; Srivastava M.; Fleming P.J., Pollard H.B., Burns A.L.; "Cloning and sequencing of the human nucleolin conA."; FEBS Lett. 250:99-105(1989).
                                                                                                                                                                                                                                                                                                                       240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFN 283
                                                                                                                                                                                                                                                                                                                                                    266 EBEBEBBVKPAPGKR-KKEMTKQKEVPEAKKQKVEGSESTTPFN 308
                                                                                                                                                                                                                                       206 INKKRPNESVSKTPVSGKKAKPAAAPAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nucleolin (Protein C23).
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Pfam: PF00076; rrm: 4.
PNOS1TE; PS50102; RRM; 4.
PROSITE; PS00030; RRM; 4.
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PIR; S04631; S04631.
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P19338;
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NUCL_HUMAN
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-! - INDUCTION: BY HEAT SHOCK.
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P41777;
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-!- DEVELOPMENTAL STAGE: PRESENT AT HIGH LEVELS IN GROWING CELLS BUT
DECREASES DRAMATICALLY DURING THE EARLY HOURS OF DEVELOPMENT.
                                                                                                                                                6 VAVTP-KNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGG-----AKLVIGTLS 58
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat; RNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.9%; Score 205; DB 1; Length 706; 27.2%; Pred. No. 0.00019; Live 29; Mismatches 95; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
12 kDa heat shock protein (4-1 protein).
HSPC ON HSP32.
Dictyostelium discoideum (Slime mold).
Eukaryota: Mycetozoa; Dictyostelium.
                                                                              ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 DESEEDDDSEKGMDVDEDDSDDDEEEDSEDEEEETPKKPEPINKKRPNESVSKTPVSGK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 EKTPEPKKVPEPKKEOVKOPTOPOOKKAAAQOPEKANNKPAAASPAKPONNOSKNAPKOP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VTANG------NAGAAVVKADTKPKAKPAEVKPAE-----EKPESDEEDESDDE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MQFFGTIVTKEEPVNLELDEGDIFHLTKAIIHPKSQGKGKVYLTA-----VISLMEED 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGESVVLSVTVGGAKLVIGTLSQD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Nucleolar phosphoprotein p130 (Nucleolar 130 kDa protein) (140 kDa nucleolar phosphoprotein) (Noppl40) (Nucleolar and coiled-body phosphoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 KAKPAAAPASTPQKTE--------KKKGGHTATPHPAKKGGKSPVNANQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 200.5; DB 1; Length 281; 21.6%; Pred. No. 0.00014; tive 49; Mismatches 123; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601
                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ASN.
2C64F57C847D7CA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 QQQQQSPAKNNNNKRPQNQNE-----NNKKKQK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 KSGGQS-SGGNNNKKPFNSGKQFGGSNNKGSNK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH NOP5 AND FIBRILLARIN.
MEDLINE-20143579; PubMed-10679015;
                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92323542; PubMed-1623516;
                                                                                                                                                                                                                                                                                                                                                                                 257 PC
265 PC
31481 MW;
                                                                                                                                                                                                                                                     EMBL; U40211; AAC47710.1; -. EMBL; L39778; AAA99510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 21.6
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                     DictyDb; DD01076; hspC
                                                                                                                                                                                                                                                                                                                                                                                                                262
281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10116;
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Yang Y., Isaac C., Wang C., Draqon F., Pogacic V., Meler U.T.; "Conserved composition of mammalian box H/ACA and box C/D small nucleolar ribonucleoprotein particles and their interaction with the
            common factor Nopp140.";
Mol. Biol. Cell 11:567-577(2000).
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15; Gaps IGYKSP------NIEQDDFTSSDDEDVP----EAVPA-PAPTAVTANGN- 126 314 VGAQSPKKAAAQTQPADSSADSSEESDSSSEEKKTPAKTVVSKTPAKPAPVKKKAESSS 373 -----AEEKPESDFEDES 160 DDEDE--SEEDDDSEKGMDVDE------198 492 TPKKPEPINKKRPNESVSK-TPVSGKKAKPAAAPASTPQKT--EKKKGGHTATPHPAKKG 255 TPPKP-PAKKKAAGAAVPKPTPVKKAAAESSSSSSSSSEDSSEERKKPKSKATPKP-QAG 550 374 DSSDSDSSEDEAPAKPVSATKSPLSKPAVTPKPPAAKAVATPKQPAGSGQKPQSRKADSS 434 SSERESSSSEEEATKKSVTTPKARVTAKAAPSLPAKQAPRAGGDSSSD-SESSSSEEEKK GKSPVNANQSPKSGGQS----SGGNNNKKPFNSGKQFGGSNNKGSNKGKGKGR 304 11.8%; Score 188; DB 1; Length 704; 26.6%; Pred. No. 0.0015; 85; Indels ------AGAAVVKADTKPKAKPAEV-KP----38; Mismatches Conservative Similarity Local Sim-Query Match Matches 83 193 127 8 음 ò 9 à q ò 셤 ð

14DF1BF2DE483EA3 CRC64;

73562 MW;

SEQUENCE

-1 - FUNCTION: BINDS TO SINGLE-STRANDED DNA AND RNA SEQUENCES, WITH

Science 287:2185-2195(2000)

551 KANGVPASONGKAGKESEEEEDTEONKKA-----AGTKPGSGKKR 591

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RAM ANDINE-ZUISOUDS: Unbeac-10/31131;

RA Adams M.D., Celniker S.E., IL P.W., Hoskins R.A., Galle R.F.,

Radams M.D., Celniker S.E., IL P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Hedderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Hedderson S.N.,

RA Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Radion R.G., Morgers Y.-H.C., Blaze, R.G., Channe M., Heiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beson K.Y., Basu A., Baxendale J., Baytaktarolu L., Beasley E.M.,

Beson K.Y., Bancs P.V., Berman B.P., Bhandari D., Boishakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadlou E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dalike C., Davepport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dalike C., Davepport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Robb S., Dunkoy B.C.,

RA Boutis K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Dodson K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Boutis N.J., Hurston K.A., Howland T.J., Hernandez J.R., Mouck J.,

A Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Mouck J.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,

RA Munch B.E., Kodira C.D., Kraft C., Kratt C., Kratt E., Morth S.,

RA Munch B.E., Wolfun K.A., Nikon K., Nusskern D.R., Pacife J.,

RA Bolazolo M., Moy W., Morby B., Murphy I., Warzy D.M., Nelson D.I.,

RA Bolazolo M., Moy W. Murphy B., Murphy I., Warzy D.M., Nelson D.J.,

RA Bolazolo M., Woy M. A., Nikon K., Wuth D., Yang X.,

RA Bolazolo M., Wassamman D.A., Wenter E., Wang A.H., Wang X.,

RA Bolazolo M., Wassama D.A., Stupicton M., Stupski M.P., Sanith T.,

RA Bolazolo M., Wassama D.A., Wolley M., Worley D.Y., Wang S., Yao Q. A.,

RA Jeng X.-, Yang S.-, Wolly M., Wolley M., Wolley B., Wolley B.,
                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pteryyota: Neottera: Endopterygota: Diptera; Brachycera: Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                Hsu T., King D.L., Labonne C., Kafatos F.C.; A Drosophila single-strand DNA/RM-binding factor contains a high-mobility-group box and is enriched in the nucleolus."; Proc. Natl. Acad. Sci. U.S.A. 90:6488-6492(1993).
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"Isolation and characterization of cDNA clones encoding the
Drosophila homolog of the HMG-box SSRP family that recognizes
                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Single-strand recognition protein (SSRP) (Chorion-factor 5).
723 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 21:1643-1646(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
MFDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-93241947; PubMed-8479916;
                                                                                                                                                                                                                                                                                                                                         MEDLINE-93342017; PubMed-7688122;
                  005344; Q9WlJ4;
01-OCT-1994 (Rel. 30, Created)
                                                                                                                                         SSRP OR SSRP1 OR CF5 OR CG4817
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific DNA structures
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
  SSRP_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574 KRENPGIKVT-EIAKKGGEMWKELKDKSKWEDAAAKDKQRYHDEMRNYKPEAGGDSDNEK 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 EEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKK--AKPAAAPAS-----TPQKT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 EEISSVNFARSG-----GSTRSFDFEVTLKNGTVHIFSSIEKEEYAKL-FDYITOKKLHV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 PKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVD---EDDSDDDE----- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 DSDGAKKKKEKKSEKKEKKEKKHKEKERTKKPSKKKKDSGKPKRATTAFMLWLNDTRESI 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 SHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEDSLVHISQASLDCTVKSGESVVLSVTV-GGAKLVIGTLSQDKFPQISFDLVFDKEFEL 77
                                                                                                    TISSUE SPECIFICITY: EXPRESSED MOST ABUNDANTLY IN NURSE CELLS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 EK------EEDDDDGDSDEESTDEDFKPNENESDVAEETDSNVESDSDDBSDASGGGG
                                                                                                                                                                                    EMBRYOGENESIS, DECREASES DURING LARVAL STAGES AND INCREASES AGAIN IN PUPAE.
                                    SUBCELLULAR LOCATION: NUCLEAR. PARTICULARLY ABUNDANT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.8%; Score 188; DB 1; Length 723; 23.5%; Pred. No. 0.0015;
                                                                                                                                                                    DEVELOPMENTAL STAGE: ABUNDANT THROUGHOUT OOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> Y (IN REF. 1).
DE8017F75C6CA207 CRC64;
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K -> E (IN REF. 1).

G -> R (IN REF. 1).

M -> T (IN REF. 1).

V -> E (IN REF. 1).

D -> E (IN REF. 1).

1 -> Y (IN REF. 1).
HIGHEST AFFINITY FOR NUCLEOTIDES G AND U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMG BOY
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InterPro, IPR000910; HMG_12_box.
InterPro, IPR000969; Ssrcognition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00505; HMG_box; 1.
PRINTS; PR00887; SSRCGGNITION.
SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X6840B; CAA48471.1; -.
EMBL; AE003462; AAF47064.1; -.
PIR; A48217, A48217
HSSP; Q05783; 1HM21.
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428
498
504
573
723 AA;
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                                                                      NUCLEOLUS
                                                                                                                                      THE OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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CONFLICT
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CONFLICT
SEQUENCE
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 S---FDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAVT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 SLGGFEIT--PPFVLRLKCGSGPVYVSGQHLVALEEEPESEDERED-----T 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 ANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVDEDD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ASP/GLU-RICH (HIGHLY ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 KVTPEEDSLVHISQASL-DCTVKSG------ESVVLSVTVGGAKI,VIGTLSQDKFPQI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 KVDDEENE----HQLSLRTVTLGAGAKDELHVVEAEALDYEGNPTKVVLASLKMSVQPTV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO38: coordinate expression of two abundant non-ribosomal nucleolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: NUCLEAR. GENERALLY NUCLECLAR, BUT IS TRANSLOCATED TO THE NUCLEOPLASM IN CASE OF SERUM STARVATION OR TREATMENT WITH ANTICANCER DRUGS (BY SIMILARITY).
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-90206792; PubMed-2320420;

Maridor G., Nigg E.A.;

Maridor G., Nigg E.A.;

"cDNA sequences of chicken nucleolin/C23 and NO38/B23, two major nucleolar proteins.";

Nucleolar Acids Res. 18:1286-1286(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                               Maridor G., Krek W., Nigg E.A.;
"Structure and developmental expression of chicken nucleolin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 11.5%; Score 183.5; DB 1; Length 294; Local Similarity 28.7%; Pred. No. 0.0012; Los 73; Conservative 32; Mismatches 86; Indels 63;
                                                                                          Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32632 MW; BIFF89B5F2322DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PIM: PHOSPHORYLATED.
-1- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Phosphorylation; RNA-binding.
                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MET-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004301; Nucleoplasmin.
Pfam; PF03066; Nucleoplasmin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-2114180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X17200; CAA35061.1; -. PIR; S08415; DNCHFM.
                                                                                                         (Nucleolar protein NO38).
                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>--</del>
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                                                                                                                                                                                                                                                                                                                                                                                          DISCUSSION OF SEQUENCE.
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186
196
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90304215;
                                                                                                                                                                                                                     NCBI_TaxID=9031;
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SEQUENCE
 NPM_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92131136; PubMed-1734284; Finkelstein A., Kostrub C.F., Li J., Chavez D.P., Wang B.O., Fang S.M., Greenblatt J., Burton Z.F.; A cDNA encoding RAP74, a general initiation factor for transcription by RNA polymerase II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- FUNCTION: TFILE IS A GENERAL TRANSCRIPTION INITIATION FACTOR THAT BINDS TO RNA POLYMERASE II AND HELPS TO RECRUIT IT TO THE INITIATION COMPLEX IN COLLABORATION WITH TFILB. IT PROMOTES
                                                             183 SDDDEEEDSEDEEEEETP-KKP--EPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92131135; PubMed-1734283;
Aso T., Vasavada H.A., Kawaguchi T., Germino F.J., Ganguly S.,
Kitajima S., Welssman S.M., Yasukochi Y.;
"Characterization of cDNA for the large subunit of the transcription
initiation factor FFIIF.";
Nature 355:461-464(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO OTHER TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription initiation factor IIF, alpha subunit (TFIIF-alpha)
(Transcription initiation factor RAP74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; DNA-binding; Nuclear protein;
135 KICN-----ASTKRPASCCCAKTPOKKPKLSEDDEDDDEDEDDDED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 231 V -> I (IN REF. 2).
361 361 F -> L (IN REF. 2).
517 AA; 58274 MW; FOD2BE44D2F3820F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X64037; CAA45408.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; X64002; CAA45404.1; -. S20248; S20248.
                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - ! - PTM: PHOSPHORYLATED.
                                                                                                                 240 KKKGGHTATPHPAK 253
                                                                                                                                                    226 DSKKDKSLTPKTPK 239
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T02168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 189968;
                                                                                                                                                                                                                                                    T2FA_HUMAN
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13;

Caps

85;

Length 517; Indels

11.2%; Score 178.5; DB 1; 26.8%; Pred. No. 0.0036; tive 34; Mismatches 83;

Conservative

Query Match Best Local Similarity Matches 74; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vitadello M., Vetcore S., Lamar E., Chien K.R., Gorza L.;
"Neurofilament M mRNA is expressed in conduction system myocytes of
the developing and adult rabbit heart.";
J. Mol. Cell. Cardiol. 28:1833-184(1996).
-1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
-1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. 1T IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION OF INTERFILLAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILLAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILLAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                             232 PKAKKKAPLAKGGRKK--KKKKGSDDEAFEDSUDGDFKGQRVDYMSDGSSSSQEEPESKA 289
                                                                                                                                                                                               290 KAPQQEEGPKGVDEQSDSSEESEERKPEEDKEEEEEKKAPTPQEKKRKNDSSEESUSSE 349
                                                                                                                                                                                                                                                                                  :| | | | | | | | | | | | | | 350 ESDIDSEASSAFFMAKKKIPPKRERRPSGGSSRGNSRPGTPSAEGGSTSSTLRAAASKLE 409
                          VKADTK-PKAKPAEVKPAEEKPESDEE--DESDDED-------ESEEDDDSE- 173
DKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAV 131
                                                                                                                                                                       174 -----KGMDVDEDDSDDDEEE--DSEDEEEETPKKPEPINKKRPNESVSKTPVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                           222 ----GKKAKPA--AAPASTPQKTEKKKGGHTATPH-----PAKKGGKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Neurofilament medium polypeptide) (NF-M) (Fragment).
                                                                                                                                                                                                                                                                                                                                              259 ------PVNANQSPKSGGQSSGGNNNKKPFNSGK 286
                                                                                                                                                                                                                                                                                                                                                                    644 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97055255; PubMed-8899542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 247378; CAA87454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein.
NON_TER
DOMAIN <1
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P54938;
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NFM_RABIT
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                                                                                                                                                                                                                                                                                                                                         96 IEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEE--KPE 153
                                                                                                                                                                                                                                                                                                                       154 SDEEDESDDEDESEEDDDSEKGMDVDEDDSDDDE · · · · · · · · · · EEDSEDEEEETP 200
                                                                                                                                                                                                                                                                                                                                                                                 201 KKPEPINK-----KRPNESVSKTPV-----SGK-------KAKPAAAPA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                         233 STPOKTEKKKGGHTATPHPAKKGGKSPVNANQS-----PKSGGQSSGGNNNKKPFNS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Dev. 3:324-333(1989).

-1- FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANOCLEOLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE HI. IT IS THOUGHT TO PLAY A ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME ASSEMBLY.
                                                                                                                                                                              Gaps
                                                                                                                                                                                                    40 SVVLSVTVGGAKLVIGTLS-QDKFPQ--ISFDLVFDKEFELSHSGTK-ANVHFIGYKSPN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 125-650 FROM N.A.
MEDLINE-89252811; PubMed-2656405;
Calzerques-Ferrer M., Mariottini P., Curie C., Lapeyre B., Gas N.,
Amalric F., Amaldi F.,
"Nucleolin from Xenopus laevis: CDNA cloning and expression during
                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                           16;
                                                                                    O-LINKED (GLCNAC) (BY SIMILARITY).
030FDAA622889678 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rankin M.L., Heine M.A., Xiao S., Leblanc M.D., Nelson J.W., Dimario P.J.,
"A complete nucleolin cDNA sequence from Xenopus laevis.";
"Nucleic Acids Res. 21:169-169(1993).
                                                                                                                                            11.1%; Score 177; DB 1; Length 644; 23.3%; Pred. No. 0.0053; Live 49; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01 FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nucleolin (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 AA
                                          COIL 2A.
LINKER 2.
COIL 2B.
                            LINKER 12.
                CO11, 1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 GK-----QFGGSNNKGSNKGKGKGR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93181171; PubMed-8441611;
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643
33
50
72
76
197
217
                                                                                                                                     Query Match
Best Local Similarity 23.3%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 NIEQDDFTSSDDE-DVP-----EAVPAPA-PTAVTANGNAGAAVVK------ 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                   PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRM_RNP_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 DMEEDD--SSDEEVEVPVKKTPAKKTATPAKATPGKAATPGKKGATPAKNGKQAKKQESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 EEEDDSDEEAEDQKPIKNKPVAKKEKPESEEDDDDEDESEEEKAVAKKPTPAKKPAG
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARC/GLY/PHE-RICH.
PHOSPHORILATION (BY SIMILARITY).
P -> Q (IN REF. 2).
PE -> LR (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Score 177; DB 1; Length 650; 27.4%; Pred. No. 0.0053;
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           SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
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-> E (IN REF. 2).
5BF9BF09768E71B4 CRC64;
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
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                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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E
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                                                                                                                                                                   PIR; A30166; A30166.
PIR; 518874, S18874.
PIR; S30250; S30250.
HSSP; P09651; 1HA1.
InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
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Matches 55; Conservative
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165
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308
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487
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Search completed: May 2, 2002, 22:31:10

Job time: 1416 sec

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2, 2002, 22:30:22 ; Search time 113.15 Seconds (without alignments) 466.314 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 MEFWGVAVTPKNATKVTPEE........KQFGGSNNKGSNKGKGKGRA 305 562222 seqs, 172994929 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-645-337-8 1589 Title: Perfect score: Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

562222

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :

SPTREMBL_19:*
1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_nammal:*
7: Sp_nammal:*
7: Sp_phage:*
7: Sp_plant:*
7: Sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | 049209 arabidopsis | O9fn16 arabidopsis | | | | | | | - | | | | Q26711 trypanosoma | 045181 caenorhabdi | | |
|-------------------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------|
| 9 | 049209 | 09FNJ6 | Q9FVE6 | 022238 | Q9M4T5 | 024591 | Q9M4U5 | 09M4U4 | Q9M4T4 | Q9LZR5 | 094F81 | Q9M4T3 | 026711 | 045181 | O9NLA3 | 041042 |
| DB | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | Ŋ | S | S | 10 |
| % Query Match Length DB | 305 | 306 | 245 | 257 | 297 | 307 | 303 | 300 | 294 | 296 | 286 | 203 | 312 | 798 | 346 | 611 |
| guery Match | 100.0 | 99.3 | 37.4 | 37.4 | 36.1 | 34.2 | 34.0 | 33.5 | 28.5 | 28.4 | 22.9 | 16.5 | 16.2 | 14.5 | 13.2 | 13.1 |
| Score | 1589 | 1578.5 | 594 | 594 | 574 | 543.5 | 541 | 532 | 453.5 | 450.5 | 364 | 262,5 | 258 | 230 | 210.5 | 207.5 |
| Result No. | 1 | ~ | 3 | ₹ | 2 | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |

| Q99k50 mus musculu Q9qzx1 rattus norv Q9vzr7 drosophila Q9vt46 mus musculu Q9nfb6 plasmodium | Q40363 medicago sa Q9vnx6 drosophlla Q9xvs4 caenorhabdi Q95pu8 chironomus Q9v6c4 drosophila | 040947 kaposi's sa Qoxurz caenorhabdi Qoxurz caenorhabdi Qofm72 arabidopsis Qogr71 kaposi's sa Qoypa9 kaposi's sa | Ogduno kaposi's sa Qg3178 caenorhabdi P70475 rattus norv Q91708 xenopus lae Q9dum3 kaposi's sa Q19973 caenorhabdi | 0911x9 kaposi's sa 098148 kaposi's sa 036421 alcelaphine 09n328 caenorhabdi 09spq2 mus musculu 093xg9 arabidopsis 09bwn0 homo saplen 090xa6 brachydanio |
|--|---|--|--|--|
| 11 099K50 11 090ZX1 5 09VZR7 11 09CT46 5 09NFB6 | 0000 | 12 040947 5 Q9XUR2 10 Q9EM72 12 Q9QR71 12 Q9YPA9 | 0 0 | 12 091LX9 12 098148 12 098148 12 098128 11 098P02 10 093ZG9 4 098WN0 13 090XA6 |
| 707 715 570 444 2163 | 635 688 971 513 857 | 1089 1151 759 1129 416 | 976 872 1187 337 1036 | 1003 1162 1300 214 1331 477 517 1369 |
| 12.9 12.9 12.6 12.5 | 12.2 12.2 12.1 12.1 | 11.6 11.6 11.6 | | 11. 11. 11. 11. 11. 11. 11. 11. 11. 11. |
| 205.5 204.5 200.5 198.5 197 | 196.5 194.5 192.5 189 | 185 184.5 184.5 184.5 | 183 182.5 182.5 182 181 180.5 | 180 180 180 179 179 178.5 178.5 |
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ALIGNMENTS

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121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEKEDDDSEKGMDVDE 180

| QY 61 RFPQ1SFDLVFDKEFELSHSGTKANVHF1CYKSPN1EQDDFTSSDDEDVPEAVPAPAFFA Db 61 KFPQ1SFDLVFDKEFELSHSGTRANVHF1GYKSPN1EQDDFTSSDDEDVPEAVPAPAFA | DFTSSDDEDVPEAVPAPAPTA 120 |
|--|---|
| 121 | 18 |
| 181 | 24 24 24 |
| 241 | 30 |
| Db 241 KKGGHTATPHPAKKGGKSPVNANGSPKSGGQSSGGNNNKKPFNSGKOFGGSNNKGSNKGK | |
| Oy 301 GKGRA 305 | |
| | |
| RESULT 2 09FNJ6 1D 09FNJ6 PRELIMINARY; PRT | |
| AC USTNO 2: DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) | date) |
| DT 01-DEC-2001 (TrEMBLrel: 19, Las DE HISTONE DEACETYLASE LIKE PROTEI ON AMEGINER OF MAINS 7 | update) |
| on Arbuzzobo or MDD.Zz./. OS Arabidopsis thaliana (Mouse-ear OC Eukarota. Viridinjantae. Strep | |
| OC Spermatophyta; Magnollophyta; e OC eurosids II; Brassicales; Brass | fore endicots; Rosidae; |
| NCBL_TAXID=3702; RN [1] | |
| | |
| | Asamizu E., Miyajima N., |
| RT "Structural analysis of Arabidopsis to RT Sequence features of the regions of 1 | thallana chromosome 5. II. 1,044,062 bp covered by thirteen |
| <pre>RI</pre> | |
| RP SEQUENCE FROM N.A. | u de maria |
| RA Nguyen M., Marlin-Neumann G., S RA Palm C.J., Bowser I., Jones T., DA Choub D Church M. Harmanhian | Lam B., Miranda M., ininci P., Chen H., |
| AA Cheux A., Chung A.A., Mayashiza RA Kim C., Lin J., Liu S.X., Narus RA Sakurai T., Satou M., Seki M., | . U., namija A., nawai U., P.K., Sakano H., ada K., Shinozaki K., |
| RA Ecker J., Theologis A., Davis R. | ייין דיין דיין דיין דיין דיין דיין דיין |
| DR EMBL: AB006699; BAB11671.1; DR EMBL: AY059893; AAL24375.1; | |
| SQ SEQUENCE 306 AA; 32348 MW; A19274D43BDD142C CRC64; | 42C CRC64; |
| Ouery Match 99.3%; Score 1578.5; D Best Local Similarity 99.7%; Pred. No. 9e-98; Matches 305; Conservative 0; Mismatches | DB 10; Length 306; ; 0; Indels 1; Gaps 1; |
| Qy 1 MEFWGVAVTPKNATKVTPEEDSLVHI | . 09 |
| | |
| | 12 |
| - | DFTSSDDEDVPEAVPAPAPTA 120 |
| QY 121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDEDESEEDDDSEKGMDVDE | SDDEDESEEDDDSEKGMDVDE 180 |

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15;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Trachcophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DDSDDEEEDSEDEEEEFTPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPOKTEE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 EDDSDDDEEEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTE 239
DDSDDDEEEDSEDEEEEFFFKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKT-E 239
                                                                                                                                         240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGQSSGGNNNKKPFNSGKQFGGSNNKGSNKG 299
                                                                                                                                                                          241 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGOSSGGNNNKKPFNSGKQFGGSNNKGSNK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEFWGVAVTPKNATKVTPEEDSLVH1SQASL-DCTVKSGESVVLSVTVGGAKLV1GTLSQ 59
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A W. K., Tian L., Malik K., Brown D., Miki B.;

W. K., Tian L., Malik K., Brown D., Miki B.;

W. K., Tian L., Malik K., Brown D., Miki B.;

W. K., Tian L., Malik K., Brown D., Miki B.;

W. K., Tian L., Malik K., Brown D., Miki B.;

Arabidopsis thaliana.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

R. Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

R. Sharits SAFOSSES, AAC28472.1;

R. SMART; SMO0355, ZAF.CZH2.1;

R. PROSITE; PSO0028; ZINC.FINGER.CZH2.2;

R. PROSITE; PSO1057; ZINC.FINGER.CZH2.2;

W. DNA-binding; Metal-binding; Zinc.finger.

SEQUENCE 245 AA; 26372 MW; E8E4F7E0A0D24F28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 245;
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01-MAR-2001 (TTEMBLTEL. 16, Last sequence update)
01-DEC-2001 (TEMBLTEL. 19, Last annotation update)
PUTATIVE HISTONE DEACETYLASE.
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50.7%; Pred. No. 2.4e-32;
tive 26; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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EMBL; AF255711; AAF70196.1; -.
InterPro; IPR000822; Znf-C2H2.
SMART; SM00355; ZnF_C2H2; 1.
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01-DEC-2001
                                                                                                                               Query Match
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A de la Bastide M.R., Parnell L.D., Kaplan N., Gnoj L., Hameed A.,
de la Bastide M.R., Parnell L.D., Kaplan N., Gnoj L., Hameed A.,
Schutz K., Hasegawa A., Gottesman T., Shohdy N., Granat S., Jensen K.,
Johnson A.F., Lodhi M., Dedhia M., Martienssen R., McCombie W.R.;
T. Lallana BAC T32N15 from chromosome V.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
R. EMBL; AC002534; AAB70032.1;
R. FAML; PRO0096; ZI-C2H2;
R. FAM, PF00096; ZI-C2H2; I.
R. SNART; SN00355; ZnF_C2H2; I.
R. ROSITE; PSS0157; ZNC_FINGER_C2H2_1; I.
R. PROSITE; PSS0157; ZNC_FINGER_C2H2_2; I.
W. DNA binding; Metal-binding; Zinc_finger.
O SEQUENCE 257 AA; 27698 MW; C44043876E6889D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 AVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEEDDDSEKGMDVD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 EDDSDDDEERDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 DKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPAPT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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"Molecular characterization of type-2 histone deacetylases in higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEFWGVAVTPKNATKVTPEEDSLVHISQASL-DCTVKSGESVVLSVTVGGAKLVIGTLSQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEFWGIEVKSGKPVTVTPEEGILIHVSQASLGECKNKKGEFVPLHVKVGNQNLVLGTLST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 EK------KKGGKA---ANQSPKSASQVSCG-SCKKTFNSGNAL-ESHNKAKH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 KKKGGHTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKKPFNSGKQFGGSNNKGSN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE HISTONE DEACETYLASE HD2.
                          01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE HISTONE DEACETYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                   37.4%; Score 594; DB 10; 50.7%; Pred. No. 2.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Mismatches
              01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                           NCBI_TaxID-3702;
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Q9M4T5;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KFPQIQFDLVFDKEFELSHTSKTASVFFSGYKVSQPAEEDEMDFDSEEVEBEEEEKIIP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 APAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEED--DDS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AP-----RANGK-----VEGKENEQKKQGKTDSSASKSKAAVNDDDDDDSAEDDSQDED 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 EKGMDVDEDDSDDDEEEDSEDE-EEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAP 231
                                                                                                                                                                                                                                                                                                                                                                                                                         61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYK-SPNIEQD--DFTS---SDDEDVPEAVP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 ASTP--QKIEKKKGGHTAIPHPAKKGGKSPVN---ANQSPKSGGQSSGGNNNKKPFNS 284
                                                                                                                                                                                                                                           30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lusser A., Brosch G., Loidl A., Haas H., Loidl P.;
"Identification of maize histone deacetylase HD2 as an acidic nucleolar phosphoprotein.";
Science 277:88-91(1997).
                                                                                                                                                                                    36.1%; Score 574; DB 10; Length 297; 46.0%; Pred. No. 6.2e-31;
                                                                                                                                                                                                                                              93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brosch G., Lusser A., Loidl P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U82815; AAB63262.1; -.
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 297 AA; 32502 MM; EEB3AAC0D2C41C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 05, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                           38; Mismatches
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InterPro; IPR000822; Znf-C2H2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
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MEDLINE-97349336; PubMed-9204905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Panicoideae; Andropogoneae; Zea.
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Best Local Similarity 44.8'
Matches 130; Conservative
                                                                                                                                                                                                               Best_Local Similarity 46.08
Matches 137; Conservative
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SEQUENCE 307 AA; 33238
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Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                  167 EEDDDSR-KGMDVDEDDSDDDEEEDSEDEEEE--TPKKPEPINKKRPNESVSKTPVSCK 223
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                                                                                                                                                                                            179 DEDDSDDDEEDSEDEEEE--TPKKPEPINKKRPNE-SVSKTPVSGKKAKPAAAPASTP 235
                                                                                                                                                                                                                          EEGDDDSSDEDDTSDDEEEDTPTPKKPE-VGKKRPAESSVLKTPLSDKKAK VATPSS-- 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Dangl M., Brosch G., Haas H., Loidl P., Lusser A.;
"Molecular characterization of type-2 histone deacetylases in higher
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121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEED--DDSEKGMDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
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                                                                                                                                                                                                                                                                             233 QKTGGKKGAAVHVATPHPAK - - GKTIVNNDKSVKSPKSAPKSGGSVPCKP 280
                                                                                                                                                                                                                                                         236 OKTEKKKGG--HTATPHPAKKGGKSPVNANQSPKS--GGQSSGGNNNKKP 281
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DNA binding; Metal-binding; Zinc_finger.
SEQUENCE 303 AA; 32613 MW; 708E4627101BB67C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HISTONE DEACETYLASE 2 ISOFORM B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           303
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NCBI_TaxiD-4577;
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InterPro; IPR000822; Znf-C2H2.
SMART; SM00355; ZnF_C2H2; 1.
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Best Local Similarity
Matches 135; Conserv
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Q9M4U5;
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Eukaryota; Viriálplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAVPAPATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 KNPHIQFDLIFDKEFELSHTSKTTSVFFTGYKVEQPFEEDEMDLDSEDEBELNVP---A 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDESEED--DDSEKGMDV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosldae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Dangl M., Brosch G., Haas H., Loidl P., Lusser A.;
"Molecular characterization of type-2 histone deacetylases in higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 EEGDDDSSDEDDTSDDEEEDTPTPKKPEVGKKRAAESSVLKTPLSDKKAK-VATPSS--O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32457 MW; 62F6C4148EB1E1FE CRC64;
                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
HISTONE DEACETYLASE 2 ISOPORM C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 KTGGKKGAAVHVATPHPAK -- GKTIVNNDKSVKSPKSAPKSG 273
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 532; DB 10;
Pred. No. 3.9e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF254073; AAF68625.1; -. InterPro; PR000822; ZH C2412.
SMAR; SMO355; ZNC C2412.1 .. PROSITE; PS00028; ZINC_FINGER_C242_1; UNKNOWN_1.PROSITE; PS01057; ZINC_FINGER_C242_2; 1. UNKNOWN_1.DNA-binching Zinc-finger.
SRQUENCE 300 AA: 32457 MW; 62P6C4148EB1E1FF
                                                                                                                                                                                                                                            300 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 124; Conservative
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                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE FROM N.A.
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284
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays (Maize
279 KKPFNS
                                                                   283 SKTFNS
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Best Local S
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                                                                                                                                                                                                               Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
A bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nayen M.,
A Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
A Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
A Seki M., Southwick A., Ecker J.R.;
I. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR255712; AAR701971; -.
R EMBL; AR575389; AAR49605.1; -.
R EMBL; AR57589; AAR49605.1; -.
R InterPro: IPR000822; ZnF-C2H2; 1.
R PROSITE; PS00182; ZnF-C2H2; 1.
R PROSITE; PS00182; ZnF-CEH2; 1.
                                                                                                        Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S., Katabidopsis thaliana chromosome S. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 PAPAPTAVTANGNAGAAVVKADTKPKAK-----PAEVKPAEEKPESD--EEDESDDEDE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 IGTLSQDKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDEDVPEAV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 GKKAKPAAAPASTPQKTEKKKGG-HTATPHPAKKGGKSPVNANQSPKSGGQSSGGNNNKK 280
Dangl M., Brosch G., Haas H., Loidl P., Graessle S., Lusser A.; "Molecular characterization of type-2 histone deacetylases in higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEFWGVAVTPKNATKVTPEEDSLVHISQASLDCTVKSGES-----VVLSVTVGGAKLV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEFWGVEVKNGKPLHLDPGLDRLVHISQVAL-----GESKNNVTEPIQLYVTVGSDKLL 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 SEEDDDSEKGM----DVDEDDSDDDEEEDSEDEEEETPKKPEPINKKRPNESVSKTPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 NKKAK-----FVTPOKTDSKKPHVHVAYPHPSKQAGKN-----SGGGSTGETSKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.5%; Score 453.5; DB 10; Length 294; 39.5%; Pred, No. 6.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Indels
                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA binding; Metal-binding; Zinc-finger.
SEOUENCE 294 AA; 31830 MW; 7B69F3BE8324ClDl CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HISTONE DEACETYLASE-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Mismatches
                                                                              STRAIN-COLUMBIA;
MEDLINE-97471969; PubMed-9330910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 123; Conservative
                                                                                                                                                                            DNA Res. 4:215-230(1997).
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                Pl clones.
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O9LZRS;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 VPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDEDESEE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 YPPAAPKSAAKQVNFQ-----LPNEDVKAK-----QDDDADGSEEDSSDDDDSENS 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 IGTLSQDKFPQISFDLVFDKEFELSHSGTKANVHFIGYKSPNIEQDDFTSSDDED---- 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Chandlar V.L., Kaeppler S.M., Kaeppler H.F., Cone K.C.;
"Sequences from the Plant Chromatin Consortium (NSF Plant Genome
project 9975930).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.4%; Score 450.5; DB 10; Length 38.3%; Pred. No. 1e-22; ive 39; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI62506; CAB82939.1; -.
InterPro; IRR00822; Znf-C2H2.
SMART; SM00355; ZnF-C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 296 AA; 32129 MW; 4B2DAABEAAIFIE9D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HD2 TYPE HISTONE DEACETYLASE HDA106.
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Best Local Similarity 38.3%
Matches 118; Conservative
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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BURATIVE HISTONE DEACETVIASE HOLD.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KFPQISFDLVFDKEFELSHSGTKANVHFIGYKSP-----NIEQDDFTSSDDEDVPEAVP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 APAPTAVTANGNAGAAVVKADTKPKAKPAEVK-PAEEKPESDEEDE------S 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 DDEDE----EDSEDDSEKGMDVDEDDSDDEE------EDSEDE---EEEE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 DDDDDDFTTSDSDNEMSEEDDSSDEDEMSEEDDSSDEDEMSGGADPSDDSSDESGSEHTS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 APKKTDVVVGKKR---AIKAEAPYGKKAK-----SEQSSQKTGDKASTSHPAKQSIK 261
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Dangl M., Brosch G., Haas H., Loidl P., Graessle S., Lusser A.;
"Molecular characterization of type-2 histone deacetylases in higher
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                                                                                                      Bergstrom D., Springer N.M., Schmitt L.T., Guthrie E., Sidorenko L., Selinger D., Kaeppler S.M., Cone K.C.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF384633; AAK67143.1; -- SEQUENCE 286 AA: 30808 MW; E295ESCDFE4DEFIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 TPKKPE-PINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTEKKKGGHTATPHPAK----
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                                                                                                                                                                                                                                                                                                        22.9%; Score 364; DB 10; Length 286; 33,1%; Pred. No. 5.6e-17;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, AF255713; AAF70198.1; --
SKQUENCE 203 AA; 22651 MW; 69A1DA5941D7A293 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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Matches 106; Conservative
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es 80; Conserv
                                                   SEQUENCE FROM N.A.
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61 LSQ-KFPQFSIDLYLGHEFEISHNST-SSVYLJGYRTFDAFDELDEEIDSDSE----- 111
                                                      115 APAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEERPESDEEDESDEDESEEDDDSEK 174
                                                                                                                                                                 175 GMDVDEDDSDDEEEDSEDEEEEFTPKKPEPINKKRPNES--VSKTPVSGKKAKPAAAPA 232
                                                                                                                                                                                                    62 FPQISFDLVFDKEFELSHSGT-KANVHFIGYKSPNIEQDDFTSSDDEDVPEA-----V 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 P----APAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDDEDES 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 EEDDDSEKGMDVDEDDSDDDEEEDSEDEEEEFTPKKPEPINKKRPNESVSKTPVSGKKAK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KGGHTATPHPAKKGGKSPVNANQSPKSG 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-EATRO 164;
MEDLINE-96279091; PubMed-8663171;
Das A., Peterson G.C., Kanner S.B., Frevert U., Parsons M.;
"A major tyrosine-phosphorylated protein of Trypanosoma brucel incleolar RNA-binding protein.";
J. Biol. Chem. 271:15675-15681(1996).
EMBL; U33863; AAC47134.1;
SEQUENCE 312 AA; 33222 MW; ZABBEDBD4416EB00 CRC64;
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                                                                                                             -----LDEYMEQQIAALPQNEINPEEDDESDSD-----
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                               233 STPQKTEKKKGGHTATPHP 251
                                                                                                                                                                                                                                                                                                                                      184 -----NKSSGGKKRCPFP 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma brucet.
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                                                                                                             112 -----
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01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 DVPEAVPAPAPTAVTANGNAGAAVVKADTKPKAKPAEVKPAEEKPESDEEDESDEDESE 167
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                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
Fulton B., Hawkins J., Gattung S., Wohldmann P., Elliott G.,
"The sequence of C. elegans cosmid K07H8.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2001 (TrEMBLrel. 19, Last annotation update)
NUCLEIC ACID-ASSOCIATED PROTEIN 36.
Asterina pectinifera (Starfish).
Eukaryota: Metazoa: Echinodermata; Eleutherozoa: Asterozoa;
Asteroidea: Valvatacea; Valvatida; Asteriniae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 14.5%; Score 230; DB 5; Length 798; Best Local Similarity 31.7%; Pred. No. 1.4e-07; Matches 72; Conservative 32; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, RAG4/659; AAC04430.1; ... InterPro; IPR002106; AA_TRNA_ligase_II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6209063CD13FAB26 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1
PROSITE; PS50102; RRM; 1.
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                                                                                                                                                           MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 798 AA; 86819 MW;
               HYPOTHETICAL 86.8 KDA PROTEIN
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                                             Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00360; RRM;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                              NCB1_TaxID-6239;
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               Nakajima H., Matoba K., Matsumoto Y., Hongo T., Kiritaka K., Sugino H., Matoba K., Hamaguchi Y., Ikegami S.; Sugino H., Nagamatsu Y., Hamaguchi Y., Ikegami S.; Sugino H., Nagamatsu Y., Hamaguchi Y., Ikegami S.; Maracterization of a novel nucleolar protein in starfish cocytes which is phosphorylated before and during oocyte maturation.*; Eur. J. Biochem. 267:295-304(2000).

EMBL; AB00304; BA90837.1; -.

Enter Proj IPR004301; Nucleoplasmin.

Fram; PF03066; Nucleoplasmin. 1.

SEQUENCE 346 AA; 39005 MW; BA88FC06167E2FDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDDDEEEDSEDEEEEETPKKPEPINKKRPNESVSKTPVSGKKAKPAAAPASTPQKTEKKK 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 SPNIEQDDFTSSDDEDVPEAVPAPAPTAVTANGNAGAAVVKADTKP-------KAKPA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 MIEISADDEEELEEDDEEE----EEEDEVEVNASPDLPVAKSKKRPLSTSDGTAKKTKMA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 EVKPAEEKPESDEEDESD------DEDESBEDD------DSEKGMDVDEDD 182
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      6 FWGDSLTGTKKEVKWNPSLDDEDDFDNLDSDCIQHFLFLKQAVLGANAKEGERNVVE---
                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                  13.2%; Score 210.5; DB 5; Length 346; 26.8%; Pred. No. 1.1e-06; tive 34; Mismatches 123; Indels 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 GGAKLVIGTLSQD----KFPQISFDLVFDKEFELSHSGTKANVHFI
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MEDLINE-20098505; PubMed-10632699;
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Best Local Similarity 26.89
Matches 91; Conservative
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